

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
13 November 2003 (13.11.2003)

PCT

(10) International Publication Number
WO 03/093464 A1

(51) International Patent Classification⁷: C12N 9/10, 9/02,
5/14, 15/82, C07K 14/415, A01H 5/00

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(21) International Application Number: PCT/NZ03/00081

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(22) International Filing Date: 6 May 2003 (06.05.2003)

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU,
AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU,
CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC,
LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW,
MX, MZ, NI, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD,
SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US,
UZ, VC, VN, YU, ZA, ZM, ZW.

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data:

60/378,930 6 May 2002 (06.05.2002) US
60/408,782 5 September 2002 (05.09.2002) US

(84) Designated States (*regional*): ARIPO patent (GH, GM,
KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW),
Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM),
European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE,
ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO,
SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM,
GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

(72) Inventors; and

Published:
— with international search report
— before the expiration of the time limit for amending the
claims and to be republished in the event of receipt of
amendments

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For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

A1

(54) Title: COMPOSITIONS ISOLATED FROM FORAGE GRASSES AND METHODS FOR THEIR USE

(57) Abstract: Isolated polynucleotides encoding polypeptides active in the fructan, cellulose, starch and/or tannin biosynthetic pathways are provided, together with expression vectors and host cells comprising such isolated polynucleotides. Methods for the use of such polynucleotides and polypeptides are also provided.

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COMPOSITIONS ISOLATED FROM FORAGE GRASSES
AND METHODS FOR THEIR USE

5 Technical Field of the Invention

This invention relates to polynucleotides isolated from forage grass tissues, specifically from *Lolium perenne* (perennial ryegrass) and *Festuca arundinacea* (tall fescue), as well as oligonucleotide probes and primers, genetic constructs comprising the polynucleotides, biological materials (including host cells and plants) incorporating the 10 polynucleotides, polypeptides encoded by the polynucleotides, and methods for using the polynucleotides and polypeptides. More particularly, the invention relates to polypeptides involved in the tannin, cellulose and fructan biosynthetic pathways, and to polynucleotides encoding such polypeptides.

15 Background of the Invention

Over the past 50 years, there have been substantial improvements in the genetic production potential of ruminant animals (sheep, cattle and deer). Levels of meat, milk or fiber production that equal an animal's genetic potential may be attained within controlled feeding systems, where animals are fully fed with energy dense, conserved forages and 20 grains. However, the majority of temperate farming systems worldwide rely on the *in situ* grazing of pastures. Nutritional constraints associated with temperate pastures can prevent the full expression of an animal's genetic potential. This is illustrated by a comparison between milk production by North American grain-fed dairy cows and New Zealand pasture-fed cattle. North American dairy cattle produce, on average, twice the milk volume of 25 New Zealand cattle, yet the genetic base is similar within both systems (New Zealand Dairy Board and United States Department of Agriculture figures). Significant potential therefore exists to improve the efficiency of conversion of pasture nutrients to animal products through the correction of nutritional constraints associated with pastures.

30 **Carbohydrate metabolism**

Plant carbohydrates can be divided into two groups depending on their function

within the plant. Structural carbohydrates, such as cellulose and lignin, are usually part of the extracellular matrix. Non-structural, storage carbohydrates act as either long- or short-term carbohydrate stores. Examples of non-structural carbohydrates include starch, sucrose and fructans.

5 Fructans are polymers that are stored in the vacuole and that consist of linear and branched chains of fructose units (for review see Vijn and Smeekens *Plant Physiol.* 120:351-359, 1999). They play an important role in assimilate partitioning and possibly in stress tolerance in many plant families. Grasses use fructans instead of starch as a water-soluble carbohydrate store (Pollock *et al.*, in "Regulation of primary metabolic pathways in plants",
10 N.J. Kruger *et al.* (eds), Kluwer Academic Publishers, The Netherlands, pp195-226, 1999). Increasing the amount of fructans and sucrose in forage crops leads to an increase in the level of water-soluble carbohydrates and thereby enhances the nutritional value of the plants. In addition, increasing the amount of fructans in forage plants decreases methane production in
15 animals fed the plants, thereby leading to lower greenhouse gas emissions, and decreases urea production in animals as less protein is degraded in the rumen (Biggs and Hancock *Trends in Plant Sci.*, 6:8-9, 2001). Fructans have also been implicated in protecting plants against water deficits caused by drought or low temperatures. Introduction of enzymes involved in the fructan biosynthetic pathway into plants that do not naturally synthesize fructans may be employed to confer cold tolerance and drought tolerance (Pilon-Smits, *Plant Physiol.* 107:125-130, 1995).

The number of fructose units within a fructan chain is referred to as the degree of polymerization (DP). In grasses, fructans of DP 6-10 are common. Such fructans of low DP are naturally sweet and are therefore of interest for use as sweeteners in foodstuffs. Long fructan chains form emulsions with a fat-like texture and a neutral taste. The human
25 digestive system is unable to degrade fructans, and fructans of high DP may therefore be used as low-calorie food ingredients. Over-expression of enzymes involved in the fructan biosynthetic pathway may be usefully employed to produce quantities of fructans that can be purified for human consumption.

Five major classes of structurally different fructans have been identified in plants,
30 with each class showing a different linkage of the fructosyl residues. Fructans found in grasses are of the mixed levan class, consisting of both (2-1)- and (2-6)-linked beta-D-

fructosyl units (Pollock *et al.*, in "Regulation of primary metabolic pathways in plants", N.J. Kruger *et al.* (eds), Kluwer Academic Publishers, The Netherlands, pp195-226, 1999). Fructans are synthesized by the action of fructosyltransferase enzymes on sucrose in the vacuole. These enzymes are closely related to invertases, enzymes that normally hydrolyze 5 sucrose.

Grasses use two fructosyltransferase enzymes to synthesize fructans, namely sucrose:sucrose 1-fructosyltransferase (1-SST) and sucrose:fructan 6-fructosyltransferase (6-SFT) (Pollock *et al.*, in "Regulation of primary metabolic pathways in plants", N.J. Kruger *et al.* (eds), Kluwer Academic Publishers, The Netherlands, pp195-226, 1999). 1-SST is a key 10 enzyme in plant fructan biosynthesis, while 6-SFT catalyzes the formation and extension of beta-2,6-linked fructans that is typically found in grasses. Specifically, 1-SST catalyzes the formation of 1-kestose plus glucose from sucrose, while 6-SFT catalyzes the formation of bifurcose plus glucose from sucrose plus 1-kestose and also the formation of 6-kestose plus 15 glucose from sucrose. Both enzymes can modify 1-kestose, 6-kestose and bifurcose further by adding additional fructose molecules. Over-expression of both 1-SST and 6-SFT in the same plant may be employed to produce fructans for use in human foodstuffs (Sevenier *et al.*, *Nature Biotechnology* 16:843-846; Hellewege *et al.*, *Proc. Nat. Acad. Sci., U.S.A.* 97:8699-8704). For a review of the fructan biosynthetic pathway see Vijn I. and Smeekens 20 S. *Plant Physiol.* 120:351-359, 1999.

The synthesis of sucrose from photosynthetic assimilates in plants, and therefore the availability of sucrose for use in fructan formation, is controlled, in part, by the enzymes sucrose phosphate synthase (SPS) and sucrose phosphate phosphatase (SPP). Sucrose plays an important role in plant growth and development, and is a major end product of photosynthesis. It also functions as a primary transport sugar and in some cases as a direct or 25 indirect regulator of gene expression (for review see Smeekens *Curr. Opin. Plant Biol.* 1:230-234, 1998). SPS regulates the synthesis of sucrose by regulating carbon partitioning in the leaves of plants and therefore plays a major role as a limiting factor in the export of photoassimilates out of the leaf. The activity of SPS is regulated by phosphorylation and moderated by concentration of metabolites and light (Huber *et al.*, *Plant Physiol.* 95:291-297, 30 1991). Specifically, SPS catalyzes the transfer of glucose from UDP-glucose to fructose-6-phosphate, thereby forming sucrose-6-phosphate (Suc-6-P). Suc-6-P is then

dephosphorylated by SPP to form sucrose (Lunn *et al.*, *Proc. Nat. Acad. Sci., U.S.A.* 97:12914-12919, 2000). The enzymes SPS and SPP exist as a heterotetramer in the cytoplasm of mesophyll cells in leaves, with SPP functioning to regulate SPS activity. SPS is also important in ripening fruits, sprouting tubers and germinating seeds (Laporte *et al.* 5 *Planta* 212:817-822, 2001).

Once in the vacuole, sucrose can be converted into fructan by fructosyltransferases as discussed above, or hydrolyzed into glucose and fructose by the hydrolase enzymes known as invertases (Sturm, *Plant Physiol.* 121:1-7, 1999). There are several different types of invertases, namely extracellular (cell wall), vacuolar (soluble acid) and cytoplasmic, with at 10 least two isoforms of each type of invertase normally being found within a plant species. In addition to having different subcellular locations, the different types of invertases have different biochemical properties. For example, soluble and cell wall invertases operate at acidic pH, whereas cytoplasmic invertases work at a more neutral or alkaline pH. Invertases are believed to regulate the entry of sucrose into different utilization pathways (Grof and 15 Campbell *Aust. J. Plant Physiol.* 28:1-12, 2001). Reduced invertase activity may increase the level of water-soluble carbohydrates in plants. Plants contain several isoforms of cell wall invertases (CWINV), which accumulate as soluble proteins. CWINV plays an important role in phloem unloading and in stress response. *Arabidopsis* contains 9 putative cytoplasmic 20 or neutral invertases that are expressed in all tissues and at all developmental stages implying a more general function than the differentially expressed acid invertases. The neutral invertase cloned from carrot and *Lolium temulentum* show no similarity to acid invertases with the exception of a conserved pentapeptide motif in the grass cDNA (Gallagher *J. Exp. Bot.* 49:789, 1998; Sturm, A. *et al.*, *Physiologia Plantarum*, 107:159-265, 1999).

Another enzyme that acts upon sucrose in plants is soluble sucrose synthase (SUS). 25 Recent results indicate that SUS is localized in the cytosol, associated with the plasma membrane and the actin cytoskeleton. Phosphorylation of SUS is one of the factors controlling localization of the enzyme (Winter and Huber, *Crit. Rev. Biochem. Mol. Biol.* 35:253-89, 2000). It catalyzes the transfer of glucose from sucrose to UDP, yielding UDP-glucose and fructose. Increasing the amount of SUS in a plant increases the amount of 30 cellulose synthesis, whereas decreasing SUS activity should increase fructan levels. Increased SUS concentration may also increase the yield of fruiting bodies. SUS activity is

highest in carbon sink tissues in plants and low in photosynthetic source tissues, and studies have indicated that SUS is the main sucrose-cleaving activity in sink tissues. Grasses have two isoforms of SUS that are encoded by separate genes. These genes are differentially expressed in different tissues.

5 Pyrophosphate-fructose 6-phosphate 1-phosphotransferase (PFP, EC 2.7.1.90) catalyses the reversible conversion of fructose 6-phosphate (Fru-6-P) and pyrophosphate (Pp_i) to fructose 1,6-bisphosphate (Fru-1,6-P) and inorganic phosphate (P_i). In the plant PFP has important physiological roles in glycosylation, sucrose metabolism, respiratory carbon flow, as well as being a supply of PP_i . Along with FBPase and PFK, PFP regulates this step
10 in the pathway of sucrose metabolism. PFP is a cytoplasmic enzyme consisting of a 250kDa tetramer (two alpha and two beta chains) with the two subunits containing all of the regulatory and catalytical functions, respectively. In the plant cell fructose 2-6-bisphosphate is a potent activator of PFP activity. In sugarcane (a C₄ grass), PFP activity is inversely correlated with sucrose content (Whittaker and Botha *Plant Physiol.*, 115, 1651-1659, 1997),
15 indicating that a reduction of PFP enzyme levels will increase the flux of sucrose synthesis. In forage grasses reducing PFP levels in the leaves will increase water-soluble carbohydrate levels in the leaf tissue. The *Arabidopsis* genome contains four closely related PFP genes thought to encode two isoforms of each subunit, however, only 1 cDNA representing each unit of the purified protein has been isolated from Castor Bean, Potato and Spinach (Todd,
20 Blakeley and Dennis *Gene*, 152, 181-186, 1995; Carlisle, Blakeley, Hemmingsen, Trevanion, Hiyoshi, Kruger and Dennis *J. Biol. Chem.*, 265, 18366-18371, 1990).

Sucrose Transporters (SUTs) play a major role in the partitioning of disaccharides (sucrose) across membranes (for a review see Williams et al., *Trends Plant Sci.*, 5:283-290, 2000). In particular SUTs are involved in loading and unloading of sucrose into the phloem
25 and the source-sink relationship within the plant. SUTs are energy dependent and can transport sucrose across large sucrose gradients. In *Arabidopsis* six SUTs have been identified, however in monocots and dicots SUTs form distinct groups. In general, monocots have 2 types of SUTs. For example barley and maize have two SUT proteins, known as SUT1 and SUT2. SUT1 is found in source, not sink, tissues, whereas SUT2 is constitutively expressed at similar levels in all tissues (Hirose, Imaizumi, Scofield, Furbank and Ohsugi *Plant Cell Physiol.* 38: 1389-1396; 1997; Weschke, et al., *Plant Journal* 21, 455-457, 2000).

Inhibition of SUT1 in potato plants by antisense technology resulted in increased levels of sucrose and starch in the source leaves (Schulz et al. *Planta*, 206, 533-543, 1998). Repressing SUT activity in forage grasses to lower phloem loading in source tissues will increase water soluble carbohydrate content in the leaves.

5

Cellulose synthesis

The major source of dietary fibre for grazing animals comes from plant cell walls. Mammals possess no enzymes capable for breaking down the polysaccharides in plant cell walls. Instead animals such as ruminants depend on microbial breakdown of plant cell walls through fermentation in either the rumen or large intestine.

Fibre in plants is measured using the Neutral Detergent Fibre (NDF) technique in which plant samples are boiled in a solution containing sodium lauryl sulfate (van Soest in "Nutritional Ecology of the Ruminant". Cornell University Press, Ithaca, NY, 1994). This detergent extracts water-soluble components such as sugars, lipids and organic acids. The remaining insoluble residue (fibre) is termed NDF and consists predominantly of plant cell wall components such as cellulose, hemicellulose, and lignin. The amount of cellulose and lignin in cell walls can be determined using the Acid Detergent Fibre (ADF) method where plant samples are boiled in sulfuric acid and sodium lauryl sulfate. The difference between NDF and ADF for a plant sample is normally considered to be the amount of hemicellulose (van Soest in "Nutritional Ecology of the Ruminant". Cornell University Press, Ithaca, NY, 1994).

Stems of most forage species have greater NDF content than leaves. For example, for a temperate C₃ grass in mid-flowering such as tall fescue (*Festuca arundinacea*), NDF content of leaves and stems is 50 and 70%, respectively (Buxton & Redfearn *J. Nutrition* 127:S814-S818, 1997). In contrast, for a C₄ tropical grass such as switchgrass (*Panicum virgatum* L.) the NDF content of leaves and stems is 70 and 85%, respectively. The digestibility of a forage is determined by cell wall content, so that legumes are more digestible than grasses because they contain less NDF. The NDF of a legume, however, is generally less digestible than that of grasses because a higher proportion of the NDF is made up by lignin. The increase of lignin as a component of NDF is also responsible for the decrease in digestibility of grasses at the time of flowering. In fact, ruminants can digest

only 40-50% of NDF in legumes compared to 60-70% for grass NDF (Buxton & Redfearn *J. Nutrition* 127:S814-S818, 1997). Digestibility of cellulose by ruminants is therefore directly related to the extent of lignification. Generally hemicellulose is more digestible than cellulose.

5 Cellulose is the most abundant carbohydrate in forage making up to 20-40% of dry matter (van Soest *in* "Nutritional Ecology of the Ruminant". Cornell University Press, Ithaca, NY, 1994). The cellulose in forages consists predominantly of β 1-4 glucan (85%) and smaller amounts of pentosans (e.g. xylose and arabinose; 15%). There appear to be two pools of cellulose within the plant cell wall, the difference being one is lignified and the other
10 is not (van Soest *in* "Nutritional Ecology of the Ruminant". Cornell University Press, Ithaca, NY, 1994). The lignified cellulose is mostly found in the primary cell wall and in the S1 outer layer of the secondary cell wall. Independent of lignification, it appears that cellulose possesses a variability in nutritive quality (van Soest *in* "Nutritional Ecology of the Ruminant". Cornell University Press, Ithaca, NY, 1994). This indicates that it is possible to
15 alter the rate of cellulose digestibility by modifying the chemical composition of cellulose. This could be achieved through manipulating the actions of the cellulose synthesis and cellulose synthesis-like enzymes found in plant cells. One method to increase digestibility in this way is to increase the activity of the cellulose synthesis and cellulose synthesis-like enzymes responsible for synthesizing hemicellulose or to down regulate the cellulose
20 synthesis and cellulose synthesis-like enzymes making cellulose. Hemicellulose is much more digestible than cellulose and is less likely to become lignified. Another way of manipulating cell wall composition is through modifying the rate and supply of primary components required for cellulose synthesis, i.e. of β 1-4 glucan and pentosans such as xylose and arabinose. One way to achieve this is to modify the actions of soluble sucrose synthase
25 and UDP glucose pyrophosphorylase (UDP-GP) enzymes that produce the UDP-glucose required for cellulose synthesis. This may be further modified by manipulating the actions of the large and small subunits of ADP-glucose pyrophosphorylase (ADP-GP), the two enzymes that are rate-limiting steps in starch synthesis (Smith, Denyer and Martin *Ann. Rev. Plant Phys. Plant Mol. Biol.* 48:67-87, 1997).

Manipulating expression of the UDPGP and ADP-GP genes would alter the chemical composition of plant cell walls in forage plants. Altering cell wall biosynthesis therefore provides an opportunity to increase digestibility of the plant dry matter. This may be achieved by increasing the amount of carbon in the plant allocated to cellulose biosynthesis 5 at the expense of lignin biosynthesis. Alternatively, decreasing the amount of cellulose biosynthesis and increasing the amount of water-soluble carbohydrates would have a similar effect. Furthermore, specifically increasing hemicellulose levels in the plant cell walls at expense of cellulose would also increase forage digestibility. By utilizing specific promoters in combination with the UDPGP and ADP-GP genes it is possible to increase or decrease the 10 starch, cellulose and/or hemicellulose levels in the leaf or stem.

Tannin Biosynthetic Pathway

Condensed tannins are polymerized flavonoids. More specifically, tannins are composed of catechin 4-ol and catechin monomer units, and are stored in the vacuole. In 15 many temperate forage crops, such as ryegrass and fescue, foliar tissues are tannin-negative. This leads to a high initial rate of fermentation when these crops are consumed by ruminant livestock resulting in both protein degradation and production of ammonia by the livestock. These effects can be reduced by the presence of low to moderate levels of tannin. In certain other plant species, the presence of high levels of tannins reduces palatability and nutritive 20 value. Introduction of genes encoding enzymes involved in the biosynthesis of condensed tannins into a plant may be employed to synthesize flavonoid compounds that are not normally made in the plant. These compounds may then be isolated and used for treating human or animal disorders or as food additives.

Much of the biosynthetic pathway for condensed tannins is shared with that for 25 anthocyanins, which are pigments responsible for flower color. Therefore, modulation of the levels of enzymes involved in the tannin biosynthetic pathway may be employed to alter the color of foliage and the pigments produced in flowers.

Most tannins described to date contain pro-cyanidin units derived from dihydroquercetin and pro-delphinidin units derived from dihydromyricetin. However, some 30 tannins contain pro-pelargonidin units derived from dihydrokaempferol. The initial step in the tannin biosynthetic pathway is the condensation of coumaryl CoA with malonyl CoA to

give naringenin-chalcone, which is catalyzed by the enzyme chalcone synthase (CHS). The enzyme chalcone isomerase (CHI) catalyzes the isomerization of naringenin chalcone to naringenin (also known as flavanone), which is then hydroxylated by the action of the enzyme flavonone 3- beta-hydroxylase (F3 β H) to give dihydrokaempferol. The enzyme 5 flavonoid 3'-hydroxylase (F3'OH) catalyzes the conversion of dihydrokaempferol to dihydroquercetin, which in turn can be converted into dihydromyricetin by the action of flavonoid 3'5'-hydroxylase (F3'5'OH). F3'OH is a P450 enzyme responsible for the brick red to orange pelargonidin-based pigments, whereas F3'5'OH is responsible for the purple and blue delphinidin-based pigments. The enzyme dihydroflavonol-4-reductase (DFR) 10 catalyzes the last step before dihydrokaempferol, dihydroquercetin and dihydromyricetin are committed for either anthocyanin (flower pigment) or proanthocyanidin (condensed tannin) formation. DFR also converts dihydrokaempferol to afzelchin-4-ol, dihydroquercetin to catechin-4-ol, and dihydromyricetin to gallocatechin-4-ol, probably by the action of more than one isoform. For a review of the tannin biosynthetic pathway, see, Robbins M.P. and 15 Morris P. in Metabolic Engineering of Plant Secondary Metabolism, Verpoorte and Alfermann (eds), Kluwer Academic Publishers, the Netherlands, 2000. The leucoanthocyanidin dioxygenase (LDOX) enzyme belongs to the iron/ascorbate-dependent family of oxidoreductases. In maize the LDOX gene A2 is required for the oxidation of leucoanthocyanidins into anthocyanidins (Menssen, Hoehmann, Martin, Schnable, Peterson, 20 Saedler and Gierl *EMBO J.* 9:3051-3057, 1990).

While polynucleotides encoding some of the enzymes involved in the fructan, cellulose and tannin biosynthetic pathways have been isolated for certain species of plants, genes encoding many of the enzymes in a wide range of plant species have not yet been 25 identified. Thus there remains a need in the art for materials useful in the modification of fructan and tannin content and composition in plants, and for methods for their use.

Summary of the Invention

The present invention provides enzymes involved in the fructan, cellulose, starch 30 and/or tannin biosynthetic pathways that are encoded by polynucleotides isolated from forage grass tissues. The polynucleotides were isolated from *Lolium perenne* (perennial ryegrass)

and *Festuca arundinacea* (tall fescue) tissues taken at different times of the year, specifically in winter and spring, and from different parts of the plants, including: leaf blades, leaf base, pseudostems, roots and stems. Genetic constructs, expression vectors and host cells comprising the inventive polynucleotides are also provided, together with methods for using 5 the inventive polynucleotides and genetic constructs to modulate the biosynthesis of fructans and tannins.

In specific embodiments, the isolated polynucleotides of the present invention comprise a sequence selected from the group consisting of: (a) SEQ ID NO: 1-44; (b) complements of SEQ ID NO: 1-44; (c) reverse complements of SEQ ID NO: 1-44; (d) 10 reverse sequences of SEQ ID NO: 1-44; (e) sequences having a 99% probability of being functionally or evolutionarily related to a sequence of (a)-(d), determined as described below; and (f) sequences having at least 75%, 80%, 90%, 95% or 98% identity to a sequence of (a)-(d), the percentage identity being determined as described below. Polynucleotides comprising at least a specified number of contiguous residues ("x-mers") of any of SEQ ID 15 NO: 1-44, and oligonucleotide probes and primers corresponding to SEQ ID NO: 1-44 are also provided. All of the above polynucleotides are referred to herein as "polynucleotides of the present invention."

In further aspects, the present invention provides isolated polypeptides encoded by the inventive polynucleotides. In specific embodiments, such polypeptides comprise an 20 amino acid sequence of SEQ ID NO: 45-88. The present invention also provides polypeptides comprising a sequence having at least 75%, 80%, 90%, 95% or 98% identity to a sequence of SEQ ID NO: 45-88, wherein the polypeptide possesses the same functional activity as the polypeptide comprising a sequence of SEQ ID NO: 45-88. The present invention also contemplates isolated polypeptides comprising at least a functional portion of 25 an amino acid sequence selected from the group consisting of: (a) SEQ ID NO: 45-88; and (b) sequences having at least 75%, 80%, 90%, 95% or 98% identity to a sequence of SEQ ID NO: 45-88.

In another aspect, the present invention provides genetic constructs, or expression vectors, comprising a polynucleotide of the present invention, either alone, in combination 30 with one or more of the inventive sequences, or in combination with one or more known polynucleotides.

In certain embodiments, the present invention provides genetic constructs comprising, in the 5'-3' direction: a gene promoter sequence; an open reading frame coding for at least a functional portion of a polypeptide of the present invention; and a gene termination sequence. An open reading frame may be orientated in either a sense or anti-sense direction. Genetic 5 constructs comprising a non-coding region of a polynucleotide of the present invention or a polynucleotide complementary to a non-coding region, together with a gene promoter sequence and a gene termination sequence, are also provided. Preferably, the gene promoter and termination sequences are functional in a host cell, such as a plant cell. Most preferably, the gene promoter and termination sequences are those of the original enzyme genes but 10 others generally used in the art, such as the Cauliflower Mosaic Virus (CMV) promoter, with or without enhancers, such as the Kozak sequence or Omega enhancer, and the *Agrobacterium tumefaciens* nopaline synthase terminator may be usefully employed in the present invention. Tissue-specific promoters may be employed in order to target expression to one or more desired tissues. The construct may further include a marker for the 15 identification of transformed cells.

In a further aspect, transgenic cells, such as transgenic plant cells, comprising the genetic constructs of the present invention are provided, together with tissues and plants comprising such transgenic cells, and fruits, seeds and other products, derivatives, or progeny of such plants.

20 In yet another aspect, the present invention provides methods for modulating the fructan, cellulose, starch and/or tannin content and composition of a target organism, such as a plant, by modulating the amount and/or activity of an inventive polynucleotide or polypeptide in the organism. In certain embodiments, such methods include stably incorporating into the genome of the target plant a genetic construct of the present invention. 25 In a preferred embodiment, the target plant is a forage grass, preferably selected from the group consisting of *Lolium* and *Festuca* species, and most preferably from the group consisting of *Lolium perenne* and *Festuca arundinacea*.

30 In a related aspect, methods for producing a plant having altered fructan or tannin composition is provided. Such methods comprise modulating the amount and/or activity of an inventive polynucleotide or polypeptide in a plant cell by, for example, transforming a plant cell with a genetic construct of the present invention to provide a transgenic cell, and

cultivating the transgenic cell under conditions conducive to regeneration and mature plant growth.

In yet a further aspect, the present invention provides methods for modifying the activity of an enzyme in a target organism, such as a plant, comprising modulating the amount and/or activity of an inventive polynucleotide or polypeptide in the target organism by, for example stably incorporating into the genome of the target organism a genetic construct of the present invention. In a preferred embodiment, the target plant is a forage grass, preferably selected from the group consisting of *Lolium* and *Festuca* species, and most preferably from the group consisting of *Lolium perenne* and *Festuca arundinacea*.

10

Brief Description of the Figures

Fig. 1 shows the neutral invertase activity of the recombinant grass alkaline/neutral invertase protein AN_INV8 from *L. perenne* (amino acid sequence provided in SEQ ID NO: 56; cDNA sequence provided in SEQ ID NO: 12). Activity was measured as the µg of glucose release from cleavage of sucrose per hour at pH 7. Also shown is an empty vector negative control (pET41a).

Fig. 2 shows the PFP activity of *L. perenne* and *F. arundinacea* PFPA and PFPB subunits in coupled reactions. Amino acid sequences for *L. perenne* PFPA and PFPB are given in SEQ ID NO: 59 and 62, respectively (corresponding cDNA sequences are SEQ ID NO: 15 and 18), and amino acid sequences for *F. arundinacea* PFPA and PFPB are given in SEQ ID NO: 60 and 63, respectively (corresponding cDNA sequences are SEQ ID NO: 16 and 19). Oxidation of NADH was measured as nmoles PPi converted.

Fig. 3 shows the amino acid sequence of SEQ ID NO: 45. The conserved UTP-glucose-1-phosphate uridylyltransferase domain is underlined.

Fig. 4 shows the amino acid sequence of SEQ ID NO: 46. The conserved UTP--glucose-1-phosphate uridylyltransferase domain is underlined.

Fig. 5 shows the amino acid sequence of SEQ ID NO: 47. The conserved glycoside hydrolase, family 32 domain is underlined.

Fig. 6 shows the amino acid sequence of SEQ ID NO: 48. A transmembrane domain is underlined.

Fig. 7 shows the amino acid sequence of SEQ ID NO: 53. The signal peptide is in bold/italics.

Fig. 8 shows the amino acid sequence of SEQ ID NO: 54. The signal peptide is in bold/italics and two conserved Antifreeze protein, type I domains are underlined.

5 Fig. 9 shows the amino acid sequence of SEQ ID NO: 55. The signal peptide is in bold/italics.

Fig. 10 shows the amino acid sequence of SEQ ID NO: 56. Two transmembrane domains are double underlined.

10 Fig. 11 shows the amino acid sequence of SEQ ID NO: 57. Two transmembrane domains are double underlined.

Fig. 12 shows the amino acid sequence of SEQ ID NO: 58. Two transmembrane domains are double underlined.

15 Fig. 13 shows the amino acid sequence of SEQ ID NO: 59. The conserved phosphofructokinase domain is underlined and a transmembrane domain is double underlined.

Fig. 14 shows the amino acid sequence of SEQ ID NO: 60. The conserved phosphofructokinase domain is underlined and a transmembrane domain is double underlined.

20 Fig. 15 shows the amino acid sequence of SEQ ID NO: 61. The conserved phosphofructokinase is underlined.

Fig. 16 shows the amino acid sequence of SEQ ID NO: 62. The conserved phosphofructokinase domain is underlined.

Fig. 17 shows the amino acid sequence of SEQ ID NO: 63. The conserved phosphofructokinase domain is underlined.

25 Fig. 18 shows the amino acid sequence of SEQ ID NO: 64. The conserved glycosyl transferase, group 1 domain is underlined and two transmembrane domains are double underlined.

30 Fig. 19 shows the amino acid sequence of SEQ ID NO: 65. The conserved glycosyl transferase, group 1 domain is underlined and two transmembrane domains are double underlined.

Fig. 20 shows the amino acid sequence of SEQ ID NO: 66. The conserved substrate transporter domain is in bold and eleven transmembrane domains are double underlined.

Fig. 21 shows the amino acid sequence of SEQ ID NO: 67. Nine transmembrane domains are double underlined.

5 Fig. 22 shows the amino acid sequence of SEQ ID NO: 68. The conserved substrate transporter domain is in bold and eleven transmembrane domains are double underlined.

Fig. 23 shows the amino acid sequence of SEQ ID NO: 69. The conserved substrate transporter domain is in bold and eleven transmembrane domains are double underlined.

10 Fig. 24 shows the amino acid sequence of SEQ ID NO: 70. The conserved substrate transporter domain is in bold and eleven transmembrane domains are double underlined.

Fig. 25 shows the amino acid sequence of SEQ ID NO: 72. The conserved nucleotidyl transferase domain is in bold and three ADP-glucose pyrophosphorylase are boxed. Nine transmembrane domains are double underlined.

15 Fig. 26 shows the amino acid sequence of SEQ ID NO: 73. The conserved nucleotidyl transferase domain is in bold and three ADP-glucose pyrophosphorylase domains are boxed. A transmembrane domain is double underlined.

Fig. 27 shows the amino acid sequence of SEQ ID NO: 74. The conserved nucleotidyl transferase domain is in bold and three ADP-glucose pyrophosphorylase domains are boxed. A transmembrane domain is double underlined.

20 Fig. 28 shows the amino acid sequence of SEQ ID NO: 75. The conserved nucleotidyl transferase domain is in bold and three ADP-glucose pyrophosphorylase domains are boxed. The signal peptide is in bold/italics and a transmembrane domain is double underlined.

25 Fig. 29 shows the amino acid sequence of SEQ ID NO: 76. The conserved naringenin-chalcone synthase domain is underlined. The signal peptide is in bold/italics and a transmembrane domain is double underlined.

Fig. 30 shows the amino acid sequence of SEQ ID NO: 77. The conserved naringenin-chalcone synthase domain is underlined and two transmembrane domains are double underlined.

Fig. 31 shows the amino acid sequence of SEQ ID NO: 78. The conserved naringenin-chalcone synthase domain is underlined and two transmembrane domains are double underlined.

Fig. 32 shows the amino acid sequence of SEQ ID NO: 79. A transmembrane
5 domain is double underlined.

Fig. 33 shows the amino acid sequence of SEQ ID NO: 80. A transmembrane domain is double underlined.

Fig. 34 shows the amino acid sequence of SEQ ID NO: 81. A transmembrane domain is double underlined.

10 Fig. 35 shows the amino acid sequence of SEQ ID NO: 82. The conserved Cytochrome P450 domain is underlined and three transmembrane domains are double underlined.

Fig. 36 shows the amino acid sequence of SEQ ID NO: 83. The conserved Cytochrome P450 domain is boxed, the signal peptide is in bold and a transmembrane
15 domain is double underlined.

Fig. 37 shows the amino acid sequence of SEQ ID NO: 84. The conserved Cytochrome P450 domain is boxed and three transmembrane domains are double underlined.

Fig. 38 shows the amino acid sequence of SEQ ID NO: 85. The conserved Cytochrome P450 domain is boxed, the signal peptide is in bold/italics and three
20 transmembrane domains are double underlined.

Fig. 39 shows the amino acid sequence of SEQ ID NO: 86. The conserved Cytochrome P450 domain is boxed and three transmembrane domains are double underlined.

Fig. 40 shows the amino acid sequence of SEQ ID NO: 87. The conserved Cytochrome P450 domain is boxed, the signal peptide is in bold/italics and three
25 transmembrane domains are double underlined.

Fig. 41 shows the amino acid sequence of SEQ ID NO: 88. The conserved 2OG-Fe(II) oxygenase superfamily domain is underlined.

Detailed Description of the Invention

30 The polypeptides of the present invention, and the polynucleotides encoding such polypeptides, have activity in fructan, cellulose, starch and/or tannin biosynthetic pathways

in plants. Using the methods and materials of the present invention, the fructan, cellulose, starch and/or tannin content of a plant may be modulated by modulating expression of polynucleotides of the present invention, or by modifying the activity of the polynucleotides or polypeptides encoded by the polynucleotides. The isolated polynucleotides and 5 polypeptides of the present invention may thus be usefully employed in the correction of nutritional imbalances associated with temperate pastures and to increase the yield of animal products from pastures.

The fructan, cellulose, starch and/or tannin content of a target organism, such as a plant, may be modified, for example, by incorporating additional copies of genes encoding 10 enzymes involved in the fructan, cellulose, starch and/or tannin biosynthetic pathways into the genome of the target plant. Similarly, a modified fructan, cellulose, starch and/or tannin content can be obtained by transforming the target plant with anti-sense copies of such genes. In addition, the number of copies of genes encoding for different enzymes in the fructan, 15 cellulose, starch and tannin biosynthetic pathways can be manipulated to modify the relative amount of each monomer unit synthesized, thereby leading to the formation of fructans, cellulose, starch or tannins having altered composition.

The present invention thus provides methods for modulating the polynucleotide and/or polypeptide content and composition of an organism. In certain embodiments, such methods involve stably incorporating into the genome of the organism a genetic construct 20 comprising one or more polynucleotides of the present invention. In one embodiment, the target organism is a plant species, preferably a forage plant, more preferably a grass of the *Lolium* or *Festuca* species, and most preferably *Lolium perenne* or *Festuca arundinacea*. In related aspects, methods for producing a plant having an altered genotype or phenotype is provided, such methods comprising transforming a plant cell with a genetic construct of the 25 present invention to provide a transgenic cell, and cultivating the transgenic cell under conditions conducive to regeneration and mature plant growth. Plants having an altered genotype or phenotype as a consequence of modulation of the level or content of a polynucleotide or polypeptide of the present invention compared to a wild-type organism, as well as components (seeds, etc.) of such plants, and the progeny of such plants, are 30 contemplated by and encompassed within the present invention.

The isolated polynucleotides of the present invention additionally have utility in genome mapping, in physical mapping, and in positional cloning of genes. The polynucleotide sequences identified as SEQ ID NOS: 1-44 and their variants, may also be used to design oligonucleotide probes and primers. Oligonucleotide probes and primers have 5 sequences that are substantially complementary to the polynucleotide of interest over a certain portion of the polynucleotide, preferably over substantially the entire length of the polynucleotides. Oligonucleotide probes designed using the inventive polynucleotides may be employed to detect the presence and examine the expression patterns of genes in any organism having sufficiently similar DNA and RNA sequences in their cells using techniques 10 that are well known in the art, such as slot blot DNA hybridization techniques. Oligonucleotide primers designed using the polynucleotides of the present invention may be used for PCR amplifications. Oligonucleotide probes and primers designed using the inventive polynucleotides may also be used in connection with various microarray technologies, including the microarray technology of Affymetrix (Santa Clara, CA).

15 In a first aspect, the present invention provides isolated polynucleotide sequences identified in the attached Sequence Listing as SEQ ID NOS: 1-44, and polypeptide sequences identified in the attached Sequence Listing as SEQ ID NO: 45-88. The polynucleotides and polypeptides of the present invention have demonstrated similarity to the following polypeptides that are known to be involved in fructan, cellulose, starch and/or tannin 20 biosynthetic processes:

TABLE 1

SEQ ID NO: DNA	SEQ ID NO: polypeptide	Category	Description
1, 2	45, 46	Carbohydrate metabolism	Homolog of UDP-glucose pyrophosphorylase (EC 2.7.7.9) (UDPGP or UGPASE) which is one of the key enzymes of the carbohydrate metabolic pathway. It plays a central role as glucosyl donor in cellular metabolic pathways. UDP-glucose pyrophosphorylase catalyzes the reversible uridylyl transfer from UDP-glucose to MgPPi, forming glucose 1-phosphate and MgUTP.
3, 4	47, 48	Fructan	Homolog of Sucrose (Suc):Suc 1-fructosyl-

SEQ ID NO: DNA	SEQ ID NO: polypeptide	Category	Description
		metabolism	transferase (1-SST) isolated from <i>L. perenne</i> . 1-SST is the key enzyme in plant fructan biosynthesis and catalyzes the <i>de novo</i> fructan synthesis from sucrose. Fructans play an important role in assimilation partitioning and in stress tolerance in many plants. It contains a typical signature of the glycosyl hydrolases family 32. The glycosyl hydrolases family 32 domain signature has a consensus of HYQPxxH/NxxNDPNG, where D is the active site residue (Henrissat, <i>Biochem. J.</i> 280:309-316, 1991).
5-14	49-58	Fructan metabolism	Homolog of alkaline/neutral invertase (AN-INV) that is involved in catalyzing sucrose into hexoses for utilization as a source of carbon and energy. AN-INV belongs to the family 32 of glycosyl hydrolases. Neutral invertase is an octamer of 456 kDa with subunits of 57 kDa, whereas alkaline invertase is a 504 kDa tetramer with subunits of 126 kDa. Neutral invertase also hydrolyzes raffinose and stachyose and, therefore, is a beta-fructofuranosidase. In contrast, alkaline invertase is highly specific for sucrose (Lee and Sturm, <i>Plant Physiol.</i> 112:1513-1522, 1996).
15, 16	59, 60	Fructan metabolism	Homologue of the alpha subunit of Pyrophosphate-dependent 6-phosphofructo-1-phosphotransferase (PFPA) that plays a role in carbohydrate metabolism. PFP is involved in the first step of glycolysis in the phosphorylation of fructose 6-phosphate (Fru 6-P). PFPA acts as a regulatory protein in regulating both the catalytic activity and the Fru-2,6-P ₂ -binding affinity of the beta subunit (Siebers <i>et al.</i> , <i>J. Bacteriol.</i> 180:2137-2143, 1998).
17-19	61-63	Fructan metabolism	Homolog of the beta subunit of Pyrophosphate-dependent 6-phosphofructo-1-phosphotransferase (PFPB) which plays a role in carbohydrate metabolism. PFP is involved in the first step of glycolysis in the phosphorylation of fructose 6-phosphate (Fru-6-P). The catalytic activity of the PFP enzyme is associated with the beta subunit PFPB while

SEQ ID NO: DNA	SEQ ID NO: polypeptide	Category	Description
			PFPA acts as a regulatory protein in regulating both the catalytic activity and the Fru-2,6-P2-binding affinity of the beta subunit (Carlisle <i>et al.</i> , <i>J. Biol. Chem.</i> 265:18366-18371, 1990; Siebers <i>et al.</i> , <i>J. Bacteriol.</i> 180:2137-2143, 1998).
20, 21	64, 65	Fructan metabolism	Homologue of sucrose phosphate synthase which is involved in the sucrose synthesis pathway. Sucrose plays an important role in plant growth and development and is a major end product of photosynthesis. It also functions as a primary transport sugar and in some cases as a direct or indirect regulator of gene expression. SPS-1 regulates the synthesis of sucrose by regulating carbon partitioning in the leaves of plants and therefore plays a major role as a limiting factor in the export of photoassimilates out of the leaf. The activity of SPS is regulated by phosphorylation and moderated by concentration of metabolites and light.
22-24	66-68	Fructan metabolism	Homologue of the sugar transporter SUT1, a member of the SUT family of low- and high-affinity sucrose transporters that is involved in transport of sucrose from mature leaves via the phloem. Expression of SUT1 has also been observed in other tissues (stems and parts of flower) suggesting that SUT1 may also have other functions, such as sucrose retrieval and phloem unloading (Burkle <i>et al.</i> , <i>Plant Physiol.</i> 118:59-68, 1998).
25, 26	69, 70	Fructan metabolism	Homologue of sugar transporter SUT2, a member of the SUT family of low- and high-affinity sucrose transporters. SUT2 is more highly expressed in sink than in source leaves, is inducible by sucrose and regulates the relative activity of low- and high-affinity sucrose transport into sieve elements (Barker <i>et al.</i> , <i>Plant Cell</i> 12:1153-1164, 2000).
27	71	Fructan metabolism	Homologue of a sugar transporter, a member of the SUT family of low- and high-affinity sucrose transporters that is involved in transport of sucrose from mature leaves via the phloem.
28, 29	72, 73	Fructan	Homolog of the large subunit (LSU) of ADP-

SEQ ID NO: DNA	SEQ ID NO: polypeptide	Category	Description
		metabolism	glucose pyrophosphorylase (AGPase), which plays a role in starch biosynthesis. It catalyzes the synthesis of the activated glycosyl donor, ADP-glucose from glucose-1-phosphate and ATP. The enzyme is found in chloroplasts of leaves and amyloplasts of developing endosperm. AGPase belongs to the glucose-1-phosphate adenylyltransferase family.
30, 31	74, 75	Carbohydrate metabolism	Homolog of the small subunit (SSU) of ADP-glucose pyrophosphorylase (AGPase), which plays a role in starch biosynthesis. It catalyzes the synthesis of the activated glycosyl donor, ADP-glucose from glucose-1-phosphate and ATP. The enzyme is found in chloroplasts of leaves and amyloplasts of developing endosperm. AGPase belongs to the glucose-1-phosphate adenylyltransferase family.
32, 33	76, 77	Tannin biosynthesis	Homolog of Chalcone Synthase (CHS) which is an important enzyme in flavonoid synthesis.
34-37	78-81	Tannin metabolism	Homologue of dihydroflavonal-4-reductase (DFR) that belongs to the dihydroflavonol-4-reductases family and is involved in the flavonoid synthesis and anthocyanidins biosynthesis. Flavonoids are secondary metabolites derived from phenylalanine and acetate metabolism that perform a variety of essential functions in higher plants.
38-43	82-87	Tannin metabolism	Homologue of flavonoid 3'-hydroxylase (F3'H) which is a key enzyme in the flavonoid pathway leading to the production of the colored anthocyanins where it is involved in determination of flower coloring. Anthocyanins synthesized in plants are controlled by flavonoid 3'-hydroxylase and flavonoid 3',5'-hydroxylase which are members of the cytochrome P450 family, a large group of membrane-bound heme-containing enzymes that are involved in a range of NADPH- and O ₂ -dependent hydroxylation reactions. Plants have evolved a large number of different P450 enzymes for the synthesis of secondary metabolites. The F3'H transcript is most abundant in petals from flowers at an early stage of development and levels decline as the

SEQ ID NO: DNA	SEQ ID NO: polypeptide	Category	Description
			flower matures. Transcripts are also detected in the ovaries, sepals, peduncles, stems and anthers of the petunia plant (Brugliera <i>et al.</i> , <i>Plant J.</i> 19:441-451, 1999)
44	88	Tannin biosynthesis	Homologue of leucoanthocyanidin dioxygenase (LDOX) which is an enzyme in the flavonoid biosynthesis pathway. LDOX is expressed as a late gene in the flavonoid biosynthesis pathway.

All the polynucleotides and polypeptides provided by the present invention are isolated and purified, as those terms are commonly used in the art. Preferably, the polypeptides and polynucleotides are at least about 80% pure, more preferably at least about 5 90% pure, and most preferably at least about 99% pure.

The word "polynucleotide(s)," as used herein, means a polymeric collection of nucleotides, and includes DNA and corresponding RNA molecules and both single and double stranded molecules, including HnRNA and mRNA molecules, sense and anti-sense strands of DNA and RNA molecules, and comprehends cDNA, genomic DNA, and wholly or 10 partially synthesized polynucleotides. A polynucleotide of the present invention may be an entire gene, or any portion thereof. As used herein, a "gene" is a DNA sequence which codes for a functional protein or RNA molecule. Operable anti-sense polynucleotides may comprise a fragment of the corresponding polynucleotide, and the definition of "polynucleotide" therefore includes all operable anti-sense fragments. Anti-sense 15 polynucleotides and techniques involving anti-sense polynucleotides are well known in the art and are described, for example, in Robinson-Benion *et al.*, *Methods in Enzymol.* 254(23): 363-375, 1995 and Kawasaki *et al.*, *Artific. Organs* 20(8): 836-848, 1996.

In specific embodiments, the present invention provides isolated polynucleotides comprising a sequence of SEQ ID NO: 1-44; polynucleotides comprising variants of SEQ ID NO: 1-44; polynucleotides comprising extended sequences of SEQ ID NO: 1-44 and their variants, oligonucleotide primers and probes corresponding to the sequences set out in SEQ ID NO: 1-44 and their variants, polynucleotides comprising at least a specified number of contiguous residues of any of SEQ ID NO: 1-44 (x -mers), and polynucleotides comprising extended sequences which include portions of the sequences set out in SEQ ID NO: 1-44, all

of which are referred to herein, collectively, as "polynucleotides of the present invention." Polynucleotides that comprise complements of such polynucleotide sequences, reverse complements of such polynucleotide sequences, or reverse sequences of such polynucleotide sequences, together with variants of such sequences, are also provided.

5 The definition of the terms "complement(s)," "reverse complement(s)," and "reverse sequence(s)," as used herein, is best illustrated by the following example. For the sequence 5' AGGACC 3', the complement, reverse complement, and reverse sequence are as follows:

complement	3' TCCTGG 5'
reverse complement	3' GGTCC 5'
reverse sequence	5' CCAGGA 3'.

10 Preferably, sequences that are complements of a specifically recited polynucleotide sequence are complementary over the entire length of the specific polynucleotide sequence.

15 As used herein, the term " x -mer," with reference to a specific value of " x ," refers to a polynucleotide comprising at least a specified number (" x ") of contiguous residues of: any of the polynucleotides provided in SEQ ID NO: 1-44. The value of x may be from about 20 to about 600, depending upon the specific sequence.

20 Polynucleotides of the present invention comprehend polynucleotides comprising at least a specified number of contiguous residues (x -mers) of any of the polynucleotides identified as SEQ ID NO: 1-44, or their variants. Similarly, polypeptides of the present invention comprehend polypeptides comprising at least a specified number of contiguous residues (x -mers) of any of the polypeptides identified as SEQ ID NO: 45-88. According to preferred embodiments, the value of x is at least 20, more preferably at least 40, more preferably yet at least 60, and most preferably at least 80. Thus, polynucleotides of the present invention include polynucleotides comprising a 20-mer, a 40-mer, a 60-mer, an 80-mer, a 100-mer, a 120-mer, a 150-mer, a 180-mer, a 220-mer, a 250-mer; or a 300-mer, 25
25 400-mer, 500-mer or 600-mer of a polynucleotide provided in SEQ ID NO: 1-44, or a variant of one of the polynucleotides corresponding to the polynucleotides provided in SEQ ID NO: 1-44. Polypeptides of the present invention include polypeptides comprising a 20-mer, a 40-mer, a 60-mer, an 80-mer, a 100-mer, a 120-mer, a 150-mer, a 180-mer, a 220-mer, a 250-mer; or a 300-mer, 400-mer, 500-mer or 600-mer of a polypeptide provided in SEQ ID NO: 45-88, or a variant thereof.

The polynucleotides of the present invention were isolated by high throughput sequencing of cDNA libraries prepared from forage grass tissue collected from *Lolium perenne* and *Festuca arundinacea*. Some of the polynucleotides of the present invention may be “partial” sequences, in that they do not represent a full-length gene encoding a full-length polypeptide. Such partial sequences may be extended by analyzing and sequencing various DNA libraries using primers and/or probes and well known hybridization and/or PCR techniques. Partial sequences may be extended until an open reading frame encoding a polypeptide, a full-length polynucleotide and/or gene capable of expressing a polypeptide, or another useful portion of the genome is identified. Such extended sequences, including full-length polynucleotides and genes, are described as “corresponding to” a sequence identified as one of the sequences of SEQ ID NO: 1-44 or a variant thereof, or a portion of one of the sequences of SEQ ID NO: 1-44 or a variant thereof, when the extended polynucleotide comprises an identified sequence or its variant, or an identified contiguous portion (x -mer) of one of the sequences of SEQ ID NO: 1-44 or a variant thereof. Similarly, RNA sequences, reverse sequences, complementary sequences, anti-sense sequences and the like, corresponding to the polynucleotides of the present invention, may be routinely ascertained and obtained using the cDNA sequences identified as SEQ ID NO: 1-44.

The polynucleotides identified as SEQ ID NOS: 1-44 contain open reading frames (“ORFs”) encoding polypeptides and functional portions of polypeptides. Open reading frames may be identified using techniques that are well known in the art. These techniques include, for example, analysis for the location of known start and stop codons, most likely reading frame identification based on codon frequencies, etc. Suitable tools and software for ORF analysis are well known in the art and include, for example, GeneWise, available from The Sanger Center, Wellcome Trust Genome Campus, Hinxton, Cambridge, CB10 1SA, United Kingdom; Diogenes, available from Computational Biology Centers, University of Minnesota, Academic Health Center, UMHG Box 43 Minneapolis MN 55455; and GRAIL, available from the Informatics Group, Oak Ridge National Laboratories, Oak Ridge, Tennessee TN. Once a partial open reading frame is identified, the polynucleotide may be extended in the area of the partial open reading frame using techniques that are well known in the art until the polynucleotide for the full open reading frame is identified.

The location of ORFs (by nucleotide position) contained within SEQ ID NO: 1-44, and the corresponding amino acid sequences are provided in Table 2 below.

TABLE 2

5

SEQ ID NO: Polynucleotide	ORF	SEQ ID NO: Polypeptide
1	72-1493	45
2	66-1481	46
3	0-1607	47
4	1-1914	48
5	123-1934	49
6	0-1671	50
7	114-1979	51
8	0-737	52
9	47-1783	53
10	170-2029	54
11	113-1849	55
12	154-1818	56
13	211-1866	57
14	79-1767	58
15	76-1926	59
16	80-1930	60
17	91-1782	61
18	91-1782	62
19	84-1775	63
20	97-2994	64
21	112-3065	65
22	226-1794	66
23	0-1226	67
24	243-1811	68
25	207-1727	69
26	101-1615	70
27	108-1634	71
28	150-1718	72
29	169-1737	73
30	12-1589	74
31	5-1579	75
32	136-1332	76
33	136-1332	77
34	95-836	78
35	95-1123	79

SEQ ID NO: Polynucleotide	ORF	SEQ ID NO: Polypeptide
36	82-847	80
37	82-1104	81
38	0-1532	82
39	58-1632	83
40	0-1580	84
41	16-1596	85
42	0-1478	86
43	20-1519	87
44	117-1259	88

Once open reading frames are identified, the open reading frames may be isolated and/or synthesized. Expressible genetic constructs comprising the open reading frames and 5 suitable promoters, initiators, terminators, etc., which are well known in the art, may then be constructed. Such genetic constructs may be introduced into a host cell to express the polypeptide encoded by the open reading frame. Suitable host cells may include various prokaryotic and eukaryotic cells, including plant cells, mammalian cells, bacterial cells, algae and the like.

The polynucleotides of the present invention may be isolated by high throughput sequencing of cDNA libraries prepared from forage grass tissue, as described below in Example 1. Alternatively, oligonucleotide probes and primers based on the sequences provided in SEQ ID NO: 1-44 can be synthesized as detailed below, and used to identify positive clones in either cDNA or genomic DNA libraries from forage grass tissue cells by means of hybridization or polymerase chain reaction (PCR) techniques. Hybridization and PCR techniques suitable for use with such oligonucleotide probes are well known in the art (see, for example, Mullis *et al.*, *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich, ed., *PCR technology*, Stockton Press: NY, 1989; and Sambrook *et al.*, eds., *Molecular cloning: a laboratory manual*, 2nd ed., CSHL Press: Cold Spring Harbor, NY, 1989). In addition to DNA-DNA hybridization, DNA-RNA or RNA-RNA hybridization assays are also possible. In the first case, the mRNA from expressed genes would then be detected instead of genomic DNA or cDNA derived from mRNA of the sample. In the second case, RNA probes could be used. Artificial analogs of DNA hybridizing specifically to target

sequences could also be employed. Positive clones may be analyzed by restriction enzyme digestion, DNA sequencing or the like.

The polynucleotides of the present invention may also, or alternatively, be synthesized using techniques that are well known in the art. The polynucleotides may be 5 synthesized, for example, using automated oligonucleotide synthesizers (e.g., Beckman Oligo 1000M DNA Synthesizer; Beckman Coulter Ltd., Fullerton, CA) to obtain polynucleotide segments of up to 50 or more nucleic acids. A plurality of such polynucleotide segments may then be ligated using standard DNA manipulation techniques that are well known in the art of molecular biology. One conventional and exemplary polynucleotide synthesis 10 technique involves synthesis of a single stranded polynucleotide segment having, for example, 80 nucleic acids, and hybridizing that segment to a synthesized complementary 85 nucleic acid segment to produce a 5 nucleotide overhang. The next segment may then be synthesized in a similar fashion, with a 5 nucleotide overhang on the opposite strand. The "sticky" ends ensure proper ligation when the two portions are hybridized. In this way, a 15 complete polynucleotide of the present invention may be synthesized entirely *in vitro*.

Oligonucleotide probes and primers complementary to and/or corresponding to SEQ ID NO: 1-44 and variants of those sequences, are also comprehended by the present invention. Such oligonucleotide probes and primers are substantially complementary to the polynucleotide of interest over a certain portion of the polynucleotide. An oligonucleotide 20 probe or primer is described as "corresponding to" a polynucleotide of the present invention, including one of the sequences set out as SEQ ID NO: 1-44 or a variant thereof, if the oligonucleotide probe or primer, or its complement, is contained within one of the sequences set out as SEQ ID NOS: 1-44 or a variant of one of the specified sequences.

Two single stranded sequences are said to be substantially complementary when the 25 nucleotides of one strand, optimally aligned and compared, with the appropriate nucleotide insertions and/or deletions, pair with at least 80%, preferably at least 90% to 95%, and more preferably at least 98% to 100%, of the nucleotides of the other strand. Alternatively, substantial complementarity exists when a first DNA strand will selectively hybridize to a second DNA strand under stringent hybridization conditions.

In specific embodiments, the inventive oligonucleotide probes and/or primers 30 comprise at least about 6 contiguous residues, more preferably at least about 10 contiguous

residues, and most preferably at least about 20 contiguous residues complementary to a polynucleotide sequence of the present invention. Probes and primers of the present invention may be from about 8 to 100 base pairs in length, preferably from about 10 to 50 base pairs in length, and more preferably from about 15 to 40 base pairs in length. The 5 probes can be easily selected using procedures well known in the art, taking into account DNA-DNA hybridization stringencies, annealing and melting temperatures, potential for formation of loops, and other factors which are well known in the art. Preferred techniques for designing PCR primers are disclosed in Dieffenbach and Dyksler, *PCR Primer: a laboratory manual*, CSHL Press: Cold Spring Harbor, NY, 1995. A software program 10 suitable for designing probes, and especially for designing PCR primers, is available from Premier Biosoft International, 3786 Corina Way, Palo Alto, CA 94303-4504.

The isolated polynucleotides of the present invention also have utility in genome mapping, in physical mapping, and in positional cloning of genes.

The polynucleotides identified as SEQ ID NO: 1-44 were isolated from cDNA clones 15 and represent sequences that are expressed in the tissue from which the cDNA was prepared. RNA sequences, reverse sequences, complementary sequences, anti-sense sequences, and the like, corresponding to the polynucleotides of the present invention, may be routinely ascertained and obtained using the cDNA sequences identified as SEQ ID NO: 1-44.

Identification of genomic DNA and heterologous species DNA can be accomplished 20 by standard DNA/DNA hybridization techniques, under appropriately stringent conditions, using all or part of a polynucleotide sequence as a probe to screen an appropriate library. Alternatively, PCR techniques using oligonucleotide primers that are designed based on known genomic DNA, cDNA and protein sequences can be used to amplify and identify genomic and cDNA sequences.

In another aspect, the present invention provides isolated polypeptides encoded by the 25 above polynucleotides. As used herein, the term "polypeptide" encompasses amino acid chains of any length, including full-length proteins, wherein the amino acid residues are linked by covalent peptide bonds. The term "polypeptide encoded by a polynucleotide" as used herein, includes polypeptides encoded by a polynucleotide that comprises a partial 30 isolated polynucleotide sequence provided herein. In specific embodiments, the inventive

polypeptides comprise an amino acid sequence selected from the group consisting of SEQ ID NO: 45-88, as well as variants of such sequences.

As noted above, polypeptides of the present invention may be produced recombinantly by inserting a polynucleotide sequence encoding the polypeptide into an expression vector and expressing the polypeptide in an appropriate host. Any of a variety of expression vectors known to those of ordinary skill in the art may be employed. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a polynucleotide molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast, and higher eukaryotic cells.

Preferably, the host cells employed are plant, *E. coli*, insect, yeast, or a mammalian cell line such as COS or CHO. The polynucleotide sequences expressed in this manner may encode naturally occurring polypeptides, portions of naturally occurring polypeptides, or other variants thereof. The expressed polypeptides may be used in various assays known in the art to determine their biological activity. Such polypeptides may also be used to raise antibodies, to isolate corresponding interacting proteins or other compounds, and to quantitatively determine levels of interacting proteins or other compounds.

In a related aspect, polypeptides are provided that comprise at least a functional portion of a polypeptide having an amino acid sequence selected from the group consisting of sequences provided in SEQ ID NO: 45-88 and variants thereof. As used herein, the "functional portion" of a polypeptide is that portion which contains an active site essential for affecting the function of the polypeptide, for example, a portion of the molecule that is capable of binding one or more reactants. The active site may be made up of separate portions present on one or more polypeptide chains and will generally exhibit high binding affinity. Functional portions of a polypeptide may be identified by first preparing fragments of the polypeptide by either chemical or enzymatic digestion of the polypeptide, or by mutation analysis of the polynucleotide that encodes the polypeptide and subsequent expression of the resulting mutant polypeptides. The polypeptide fragments or mutant polypeptides are then tested to determine which portions retain biological activity, using methods well known to those of skill in the art, including the representative assays described below.

Portions and other variants of the inventive polypeptides may be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be 5 synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85: 2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied Biosystems, Inc. (Foster City, California), and may be 10 operated according to the manufacturer's instructions. Variants of a native polypeptide may be prepared using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (Kunkel, *Proc. Natl. Acad. Sci. USA* 82: 488-492, 1985). Sections of DNA sequences may also be removed using standard techniques to permit preparation of truncated polypeptides.

15 As used herein, the term "variant" comprehends nucleotide or amino acid sequences different from the specifically identified sequences, wherein one or more nucleotides or amino acid residues is deleted, substituted, or added. Variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant sequences (polynucleotide or polypeptide) preferably exhibit at least 75%, more preferably at least 80%, more preferably at 20 least 90%, more preferably yet at least 95%, and most preferably at least 98% identity to a sequence of the present invention. The percentage identity is determined by aligning the two sequences to be compared as described below, determining the number of identical residues in the aligned portion, dividing that number by the total number of residues in the inventive (queried) sequence, and multiplying the result by 100.

25 Polynucleotides and polypeptides having a specified percentage identity to a polynucleotide or polypeptide identified in one of SEQ ID NO: 1-88 thus share a high degree of similarity in their primary structure. In addition to a specified percentage identity to a polynucleotide of the present invention, variant polynucleotides and polypeptides preferably have additional structural and/or functional features in common with a polynucleotide of the 30 present invention. Polynucleotides having a specified degree of identity to, or capable of hybridizing to, a polynucleotide of the present invention preferably additionally have at least

one of the following features: (1) they contain an open reading frame, or partial open reading frame, encoding a polypeptide, or a functional portion of a polypeptide, having substantially the same functional properties as the polypeptide, or functional portion thereof, encoded by a polynucleotide in a recited SEQ ID NO:; or (2) they contain identifiable domains in common.

5 Polynucleotide or polypeptide sequences may be aligned, and percentages of identical nucleotides or amino acids in a specified region may be determined against another polynucleotide or polypeptide, using computer algorithms that are publicly available. For example, the BLASTN and FASTA algorithms, set to the default parameters described in the documentation and distributed with the algorithm, may be used for aligning and identifying
10 the similarity of polynucleotide sequences. The alignment and similarity of polypeptide sequences may be examined using the BLASTP algorithm. BLASTX and FASTX algorithms compare nucleotide query sequences translated in all reading frames against polypeptide sequences. The FASTA and FASTX algorithms are described in Pearson and Lipman, *Proc. Natl. Acad. Sci. USA* 85:2444-2448, 1988; and in Pearson, *Methods in Enzymol.* 183:63-98, 1990. The FASTA software package is available from the University of Virginia by contacting the Assistant Provost for Research, University of Virginia, PO Box 9025, Charlottesville, VA 22906-9025. The BLASTN software is available from the National Center for Biotechnology Information (NCBI), National Library of Medicine, Building 38A, Room 8N805, Bethesda, MD 20894. The BLASTN algorithm Version 2.0.11
15 [Jan-20-2000] set to the default parameters described in the documentation and distributed with the algorithm, is preferred for use in the determination of polynucleotide variants according to the present invention. The use of the BLAST family of algorithms, including BLASTN, BLASTP and BLASTX, is described in the publication of Altschul *et al.*, "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs," *Nucleic Acids Res.* 25:3389-3402, 1997.
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The following running parameters are preferred for determination of alignments and similarities using BLASTN that contribute to the percentage identity and E values for polynucleotides: Unix running command with the following default parameters: blastall -p blastn -d embldb -e 10 -G 0 -E 0 -r 1 -v 30 -b 30 -i queryseq -o results; and parameters are:
30 -p Program Name [String]; -d Database [String]; -e Expectation value (E) [Real]; -G Cost to open a gap (zero invokes default behavior) [Integer]; -FF low complexity filter; -E Cost to

extend a gap (zero invokes default behavior) [Integer]; -r Reward for a nucleotide match (BLASTN only) [Integer]; -v Number of one-line descriptions (V) [Integer]; -b Number of alignments to show (B) [Integer]; -i Query File [File In]; -o BLAST report Output File [File Out] Optional.

5 The following running parameters are preferred for determination of alignments and similarities using BLASTP that contribute to the percentage identity and E values of polypeptide sequences: blastall -p blastp -d swissprotdb -e 10 -G 0 -E 0 -FF -v 30 -b 30 -i queryseq -o results; the parameters are: -p Program Name [String]; -d Database [String]; -e Expectation value (E) [Real]; -G Cost to open a gap (zero invokes default behavior) [Integer]; -FF low complexity filter; -E Cost to extend a gap (zero invokes default behavior) [Integer]; -v Number of one-line descriptions (v) [Integer]; -b Number of alignments to show (b) [Integer]; -I Query File [File In]; -o BLAST report Output File [File Out] Optional.

10 15 The “hits” to one or more database sequences by a queried sequence produced by BLASTN, BLASTP, FASTA or a similar algorithm, align and identify similar portions of sequences. The hits are arranged in order of the degree of similarity and the length of sequence overlap. Hits to a database sequence generally represent an overlap over only a fraction of the sequence length of the queried sequence.

20 As noted above, the percentage identity of a polynucleotide or polypeptide sequence is determined by aligning polynucleotide and polypeptide sequences using appropriate algorithms, such as BLASTN or BLASTP, respectively, set to default parameters; identifying the number of identical nucleic or amino acids over the aligned portions; dividing the number of identical nucleic or amino acids by the total number of nucleic or amino acids of the polynucleotide or polypeptide of the present invention; and then multiplying by 100 to determine the percentage identity. By way of example, a queried polynucleotide having 220 nucleic acids has a hit to a polynucleotide sequence in the EMBL database having 520 nucleic acids over a stretch of 23 nucleotides in the alignment produced by the BLASTN algorithm using the default parameters. The 23-nucleotide hit includes 21 identical nucleotides, one gap and one different nucleotide. The percentage identity of the queried polynucleotide to the hit in the EMBL database is thus 21/220 times 100, or 9.5%. The 25 30 percentage identity of polypeptide sequences may be determined in a similar fashion.

The BLASTN and BLASTX algorithms also produce "Expect" values for polynucleotide and polypeptide alignments. The Expect value (E) indicates the number of hits one can "expect" to see over a certain number of contiguous sequences by chance when searching a database of a certain size. The Expect value is used as a significance threshold 5 for determining whether the hit to a database indicates true similarity. For example, an E value of 0.1 assigned to a polynucleotide hit is interpreted as meaning that in a database of the size of the EMBL database, one might expect to see 0.1 matches over the aligned portion of the sequence with a similar score simply by chance. By this criterion, the aligned and matched portions of the sequences then have a probability of 90% of being related. For 10 sequences having an E value of 0.01 or less over aligned and matched portions, the probability of finding a match by chance in the EMBL database is 1% or less using the BLASTN algorithm. E values for polypeptide sequences may be determined in a similar fashion using various polypeptide databases, such as the SwissProt database.

According to one embodiment, "variant" polynucleotides and polypeptides, with 15 reference to each of the polynucleotides and polypeptides of the present invention, preferably comprise sequences having the same number or fewer nucleotides or amino acids than each of the polynucleotides or polypeptides of the present invention and producing an E value of 0.01 or less when compared to the polynucleotide or polypeptide of the present invention. That is, a variant polynucleotide or polypeptide is any sequence that has at least a 99% 20 probability of being related to the polynucleotide or polypeptide of the present invention, measured as having an E value of 0.01 or less using the BLASTN or BLASTX algorithms set at the default parameters. According to a preferred embodiment, a variant polynucleotide is a sequence having the same number or fewer nucleic acids than a polynucleotide of the present invention that has at least a 99% probability of being related to the polynucleotide of the 25 present invention, measured as having an E value of 0.01 or less using the BLASTN algorithm set at the default parameters. Similarly, according to a preferred embodiment, a variant polypeptide is a sequence having the same number or fewer amino acids than a polypeptide of the present invention that has at least a 99% probability of being related as the polypeptide of the present invention, measured as having an E value of 0.01 or less using the 30 BLASTP algorithm set at the default parameters.

In an alternative embodiment, variant polynucleotides are sequences that hybridize to a polynucleotide of the present invention under stringent conditions. Stringent hybridization conditions for determining complementarity include salt conditions of less than about 1 M, more usually less than about 500 mM, and preferably less than about 200 mM.

5 Hybridization temperatures can be as low as 5°C, but are generally greater than about 22°C, more preferably greater than about 30°C, and most preferably greater than about 37°C. Longer DNA fragments may require higher hybridization temperatures for specific hybridization. Since the stringency of hybridization may be affected by other factors such as probe composition, presence of organic solvents, and extent of base mismatching, the
10 combination of parameters is more important than the absolute measure of any one alone. An example of "stringent conditions" is prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65°C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65°C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65°C.

15 The present invention also encompasses polynucleotides that differ from the disclosed sequences but that, as a consequence of the discrepancy of the genetic code, encode a polypeptide having similar enzymatic activity to a polypeptide encoded by a polynucleotide of the present invention. Thus, polynucleotides comprising sequences that differ from the polynucleotide sequences recited in SEQ ID NO: 1-44, or complements, reverse sequences,
20 or reverse complements of those sequences, as a result of conservative substitutions are contemplated by and encompassed within the present invention. Additionally, polynucleotides comprising sequences that differ from the polynucleotide sequences recited in SEQ ID NO: 1-44, or complements, reverse complements or reverse sequences thereof, as a result of deletions and/or insertions totaling less than 10% of the total sequence length are
25 also contemplated by and encompassed within the present invention. Similarly, polypeptides comprising sequences that differ from the polypeptide sequences recited in SEQ ID NO: 45-88 as a result of amino acid substitutions, insertions, and/or deletions totaling less than 10% of the total sequence length are contemplated by and encompassed within the present invention, provided the variant polypeptide has activity in a fructan, cellulose, starch and/or
30 tannin biosynthetic pathway.

In another aspect, the present invention provides genetic constructs comprising, in the 5'-3' direction, a gene promoter sequence; an open reading frame coding for at least a functional portion of a polypeptide of the present invention; and a gene termination sequence. The open reading frame may be orientated in either a sense or anti-sense direction. For 5 applications where amplification of fructan, cellulose, starch or tannin synthesis is desired, the open reading frame may be inserted in the construct in a sense orientation, such that transformation of a target organism with the construct will lead to an increase in the number of copies of the gene and therefore an increase in the amount of enzyme. When down-regulation of fructan, cellulose, starch or tannin synthesis is desired, the open reading frame 10 may be inserted in the construct in an anti-sense orientation, such that the RNA produced by transcription of the polynucleotide is complementary to the endogenous mRNA sequence. This, in turn, will result in a decrease in the number of copies of the gene and therefore a decrease in the amount of enzyme. Alternatively, regulation may be achieved by inserting appropriate sequences or subsequences (e.g., DNA or RNA) in ribozyme constructs.

15 Genetic constructs comprising a non-coding region of a gene coding for a polypeptide of the present invention, or a nucleotide sequence complementary to a non-coding region, together with a gene promoter sequence and a gene termination sequence, are also provided. As used herein the term "non-coding region" includes both transcribed sequences which are not translated, and non-transcribed sequences within about 2000 base pairs 5' or 3' of the 20 translated sequences or open reading frames. Examples of non-coding regions which may be usefully employed in the inventive constructs include introns and 5'-non-coding leader sequences. Transformation of a target plant with such a genetic construct may lead to a reduction in the amount of fructan, cellulose, starch or tannin synthesized by the plant by the process of cosuppression, in a manner similar to that discussed, for example, by Napoli *et al.*, 25 *Plant Cell* 2:279-290, 1990; and de Carvalho Niebel *et al.*, *Plant Cell* 7:347-358, 1995.

The genetic constructs of the present invention further comprise a gene promoter sequence and a gene termination sequence, operably linked to the polynucleotide to be transcribed, which control expression of the gene. The gene promoter sequence is generally positioned at the 5' end of the polynucleotide to be transcribed, and is employed to initiate 30 transcription of the polynucleotide. Gene promoter sequences are generally found in the 5' non-coding region of a gene but they may exist in introns (Luehrs, *Mol. Gen. Genet.*

225:81-93, 1991) or in the coding region, as for example in PAL of tomato (Bloksberg, *Studies on the Biology of Phenylalanine Ammonia Lyase and Plant Pathogen Interaction*, Ph.D. Thesis, University of California, Davis, 1991, University Microfilms International Order No. 9217564). When the construct includes an open reading frame in a sense
5 orientation, the gene promoter sequence also initiates translation of the open reading frame. For genetic constructs comprising either an open reading frame in an anti-sense orientation or a non-coding region, the gene promoter sequence consists only of a transcription initiation site having a RNA polymerase binding site.

A variety of gene promoter sequences which may be usefully employed in the genetic
10 constructs of the present invention are well known in the art. The promoter gene sequence, and also the gene termination sequence, may be endogenous to the target plant host or may be exogenous, provided the promoter is functional in the target host. For example, the promoter and termination sequences may be from other plant species, plant viruses, bacterial plasmids and the like. Preferably, gene promoter and termination sequences are from the
15 inventive sequences themselves.

Factors influencing the choice of promoter include the desired tissue specificity of the construct, and the timing of transcription and translation. For example, constitutive promoters, such as the 35S Cauliflower Mosaic Virus (CaMV 35S) promoter or the superubiquitin promoter (PCT International Patent Publication WO 00/58474), will affect the
20 activity of the enzyme in all parts of the plant. Use of a tissue specific promoter will result in production of the desired sense or anti-sense RNA only in the tissue of interest. With DNA constructs employing inducible gene promoter sequences, the rate of RNA polymerase binding and initiation can be modulated by external stimuli, such as light, heat, anaerobic stress, alteration in nutrient conditions and the like. Temporally regulated promoters can be
25 employed to effect modulation of the rate of RNA polymerase binding and initiation at a specific time during development of a transformed cell. Preferably, the original promoters from the enzyme gene in question, or promoters from a specific tissue-targeted gene in the organism to be transformed, such as *Lolium* or *Festuca*, are used. Grass promoters different from the original gene may also be usefully employed in the inventive genetic constructs in
30 order to prevent feedback inhibition. For example, the fructosyltransferase gene will be regulated by sucrose sensing systems; therefore removing the gene from under control of its

normal promoter allows the gene to be active all the time. Other examples of gene promoters which may be usefully employed in the present invention include, mannopine synthase (mas), octopine synthase (ocs) and those reviewed by Chua *et al.*, *Science* 244:174-181, 1989.

5 The gene termination sequence, which is located 3' to the polynucleotide to be transcribed, may come from the same gene as the gene promoter sequence or may be from a different gene. Many gene termination sequences known in the art may be usefully employed in the present invention, such as the 3' end of the *Agrobacterium tumefaciens* nopaline synthase gene. However, preferred gene terminator sequences are those from the
10 original enzyme gene or from the target species to be transformed.

The genetic constructs of the present invention may also contain a selection marker that is effective in plant cells, to allow for the detection of transformed cells containing the inventive construct. Such markers, which are well known in the art, typically confer resistance to one or more toxins. One example of such a marker is the NPTII gene whose
15 expression results in resistance to kanamycin or hygromycin, antibiotics which are usually toxic to plant cells at a moderate concentration (Rogers *et al.*, in Weissbach A and H, eds., *Methods for Plant Molecular Biology*, Academic Press Inc.: San Diego, CA, 1988). Alternatively, the presence of the desired construct in transformed cells can be determined by means of other techniques well known in the art, such as Southern and Western blots.

20 Techniques for operatively linking the components of the inventive genetic constructs are well known in the art and include the use of synthetic linkers containing one or more restriction endonuclease sites as described, for example, by Sambrook *et al.*, (*Molecular cloning: a laboratory manual*, CSHL Press: Cold Spring Harbor, NY, 1989). The genetic construct of the present invention may be linked to a vector having at least one replication
25 system, for example, *E. coli*, whereby after each manipulation, the resulting construct can be cloned and sequenced, and the correctness of the manipulation determined.

The genetic constructs of the present invention may be used to transform a variety of plants, both monocotyledonous (e.g., grasses, maize/corn, grains, oats, rice, sorghum, millet, rye, sugar cane, wheat and barley), dicotyledonous (e.g., *Arabidopsis*, tobacco, legumes, alfalfa, oaks, eucalyptus, maple), and gymnosperms. In a preferred embodiment, the inventive genetic constructs are employed to transform grasses. Preferably the target plant is
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selected from the group consisting of *Lolium* and *Festuca* species, most preferably from the group consisting of *Lolium perenne* and *Festuca arundinacea*. Plants that may be usefully transformed with the inventive genetic constructs include other species of ryegrass and fescue, including, but not limited to *Lolium multiflorum* (Italian ryegrass), *Lolium hybridum* 5 (hybrid ryegrass), *Lolium rigidum* (Wimerra grass), *Lolium temulentum* (darnel), *Festuca rubra* (red fescue) and *Festuca pratensis* (meadow fescue). As discussed above, transformation of a plant with a genetic construct of the present invention will produce a modified fructan, cellulose, starch or tannin content in the plant.

The production of RNA in target cells may be controlled by choice of the promoter 10 sequence, or by selecting the number of functional copies or the site of integration of the polynucleotides incorporated into the genome of the target organism. A target plant may be transformed with more than one construct of the present invention, thereby modulating the fructan, cellulose, starch and/or tannin biosynthetic pathways by affecting the activity of more than one enzyme, affecting enzyme activity in more than one tissue, or affecting 15 enzyme activity at more than one expression time. Similarly, a construct may be assembled containing more than one open reading frame coding for an enzyme encoded by a polynucleotide of the present invention or more than one non-coding region of a gene coding for such an enzyme. The polynucleotides of the present invention may also be employed in combination with other known sequences encoding enzymes involved in the lignin, fructan 20 and/or tannin biosynthetic pathways. In this manner, more than one biosynthetic pathway may be modulated, or a fructan, cellulose, starch or tannin biosynthetic pathway may be added to a plant to produce a plant having an altered phenotype.

Techniques for stably incorporating genetic constructs into the genome of target 25 plants are well known in the art and include *Agrobacterium tumefaciens* mediated introduction, electroporation, protoplast fusion, injection into reproductive organs, injection into immature embryos, high velocity projectile introduction and the like. The choice of technique will depend upon the target plant to be transformed. For example, dicotyledonous plants, and certain monocots and gymnosperms may be transformed by *Agrobacterium* Ti plasmid technology, as described, for example by Bevan, *Nucleic Acid Res.* 12:8711-8721, 30 1984. Targets for the introduction of the genetic constructs of the present invention include tissues, such as leaf tissue, disseminated cells, protoplasts, seeds, embryos, meristematic

regions; cotyledons, hypocotyls, and the like. Transformation techniques which may be usefully employed in the inventive methods include those taught by Ellis *et al.*, *Plant Cell Reports*, 8:16-20, 1989; Wilson *et al.*, *Plant Cell Reports* 7:704-707, 1989; and Tautorus *et al.*, *Theor. Appl. Genet.* 78:531-536, 1989.

Once the cells are transformed, cells having the inventive genetic construct incorporated in their genome may be selected by means of a marker, such as the kanamycin resistance marker discussed above. Transgenic cells may then be cultured in an appropriate medium to regenerate whole plants, using techniques well known in the art. In the case of protoplasts, the cell wall is allowed to reform under appropriate osmotic conditions. In the case of seeds or embryos, an appropriate germination or callus initiation medium is employed. For explants, an appropriate regeneration medium is used. Regeneration of plants is well established for many species. The resulting transformed plants may be reproduced sexually or asexually, using methods well known in the art, to give successive generations of transgenic plants.

Polynucleotides of the present invention may also be used to specifically suppress gene expression by methods that operate post-transcriptionally to block the synthesis of products of targeted genes, such as RNA interference (RNAi), and quelling. Briefly, traditional methods of gene suppression, employing anti-sense RNA or DNA, operate by binding to the reverse sequence of a gene of interest such that binding interferes with subsequent cellular processes and therefore blocks synthesis of the corresponding protein. RNAi also operates on a post-translational level and is sequence specific, but suppresses gene expression far more efficiently. Exemplary methods for controlling or modifying gene expression using RNAi are provided in US Patent 6,506,559 and PCT International Publications WO 99/49029 and WO 99/53050. In these methods, post-transcriptional gene silencing is brought about by a sequence-specific RNA degradation process which results in the rapid degradation of transcripts of sequence-related genes. Studies have shown that double-stranded RNA may act as a mediator of sequence-specific gene silencing (see, for example, Montgomery and Fire, *Trends in Genetics*, 14:255-258, 1998). Gene constructs that produce transcripts with self-complementary regions are particularly efficient at gene silencing. A unique feature of this post-transcriptional gene silencing pathway is that silencing is not limited to the cells where it is initiated. The gene-silencing effects may be

disseminated to other parts of an organism and even transmitted through the germ line to several generations.

The polynucleotides of the present invention may thus be employed to generate gene silencing constructs and/or gene-specific self-complementary RNA sequences that can be delivered by conventional art-known methods to plant tissues, such as forage grass tissues. Within genetic constructs, sense and antisense sequences can be placed in regions flanking an intron sequence in proper splicing orientation with donor and acceptor splicing sites, such that intron sequences are removed during processing of the transcript, and sense and antisense sequences, as well as splice junction sequences, bind together to form double-stranded RNA. Alternatively, spacer sequences of various lengths may be employed to separate self-complementary regions of sequence in the construct. During processing of the gene construct transcript, intron sequences are spliced-out, allowing sense and anti-sense sequences, as well as splice junction sequences, to bind forming double-stranded RNA. Select ribonucleases then bind to and cleave the double-stranded RNA, thereby initiating the cascade of events leading to degradation of specific mRNA gene sequences, and silencing specific genes. Alternatively, rather than using a gene construct to express the self-complementary RNA sequences, the gene-specific double-stranded RNA segments are delivered to one or more targeted areas to be internalized into the cell cytoplasm to exert a gene silencing effect. The double-stranded RNA must have sufficient homology to the targeted gene to mediate RNAi and is preferably at least 25 nucleotides in length. Preferably, the double-stranded RNA corresponds specifically to a polynucleotide of the present invention. Gene silencing RNA sequences comprising the polynucleotides of the present invention are useful for creating genetically modified plants with desired phenotypes as well as for characterizing genes (for example, in high-throughput screening of sequences), and studying their functions in intact organisms.

Example 1ISOLATION OF cDNA SEQUENCES FROM *L. PERENNE* AND
F. ARUNDINACEA CDNA LIBRARIES

5 *L. perenne* and *F. arundinacea* cDNA expression libraries were constructed and screened as follows. Tissue was collected from *L. perenne* and *F. arundinacea* during winter and spring, and snap-frozen in liquid nitrogen. The tissues collected included those obtained from leaves, pseudostem, roots, inflorescence (day 0), stem bases from day 7 emerged inflorescence, basal leaf day 3 and day 6, floral stem and vegetative stem. Total RNA was 10 isolated from each tissue type using TRIZol Reagent (BRL Life Technologies, Gaithersburg, MD). mRNA from each tissue type was obtained using a Poly(A) Quik mRNA isolation kit (Stratagene, La Jolla, CA), according to the manufacturer's specifications. cDNA expression libraries were constructed from the purified mRNA by reverse transcriptase synthesis followed by insertion of the resulting cDNA in Lambda ZAP using a ZAP Express cDNA 15 Synthesis Kit (Stratagene), according to the manufacturer's protocol. The resulting cDNA clones were packaged using a Gigapack II Packaging Extract (Stratagene) employing 1 µl of sample DNA from the 5 µl ligation mix. Mass excision of the libraries was performed using XL1-Blue MRF' cells and XLORL cells (Stratagene) with ExAssist helper phage (Stratagene). The excised phagemids were diluted with NZY broth (Gibco BRL, 20 Gaithersburg, MD) and plated out onto LB-kanamycin agar plates containing 5-bromo-4-chloro-3-indolyl-beta-D-galactosidase (X-gal) and isopropylthio-beta-galactoside (IPTG).

25 Of the colonies plated and picked for DNA preparations, the large majority contained an insert suitable for sequencing. Positive colonies were cultured in NZY broth with kanamycin and DNA was purified following standard protocols. Agarose gel at 1% was used to screen sequencing templates for chromosomal contamination. Dye terminator sequences were prepared using a Biomek 2000 robot (Beckman Coulter Inc., Fullerton, CA) for liquid handling and DNA amplification using a 9700 PCR machine (Perkin Elmer/Applied Biosystems, Foster City, CA) according to the manufacturer's protocol.

30 The DNA sequences for positive clones were obtained using a Perkin Elmer/Applied Biosystems Division Prism 377 sequencer. cDNA clones were sequenced from the 5' end. The polynucleotide sequences identified as SEQ ID NO: 1, 3-5, 8-15, 17, 18, 20, 25, 27, 28,

30, 36-39 and 44 were identified from *Lolium perenne* cDNA expression libraries, with the polynucleotides of SEQ ID NO: 2, 6, 7, 16, 19, 21-24, 26, 29, 31-35 and 40-43 being identified from *Festuca arundinacea* cDNA expression libraries.

5 *BLASTN Polynucleotide Analysis*

The isolated cDNA sequences were compared to sequences in the EMBL DNA database using the computer algorithm BLASTN. Comparisons of DNA sequences provided in SEQ ID NO: 1-44 to sequences in the EMBL DNA database were made as of April 28, 2003, using BLASTN algorithm Version 2.0.11 [Jan-20-2000], and the following Unix 10 running command: blastall -p blastn -d embldb -e 10 -FF -G0 -E0 -r 1 -v 30 -b 30 -i queryseq -o.

The sequences of SEQ ID NO: 6-9, 11-19, 21, 25-27 and 34-44 were determined to have less than 50% identity, determined as described above using the computer algorithm BLASTN, to sequences in the EMBL database. The sequence of SEQ ID NO: 3, 4, 10, 20, 15 22-24, 28, 29 and 31-33 was determined to have less than 75% identity, determined as described above, to sequences in the EMBL database, using the computer algorithm BLASTN, as described above. The sequences of SEQ ID NO: 1, 2 and 30 were determined to have less than 90% identity to sequences in the EMBL database using the computer algorithm BLASTN, as described above. Finally, the sequence of SEQ ID NO: 5 were 20 determined to have less than 98% identity to sequences in the EMBL database using the computer algorithm BLASTN, as described above.

BLASTP Polypeptide Analysis

The isolated sequences were compared to sequences in the SwissProt protein database 25 using the computer algorithm BLASTP. Specifically, comparisons of polypeptide sequences provided in SEQ ID NO: 45-88 to sequences in the SwissProt protein database were made as of April 28, 2003, using BLASTP algorithm Version 2.0.11 [Jan-20-2000], and the following Unix running command: blastall -p blastp -d swissprot -e 10 -FF -G0 -E0 -v 30 -b 30 -i queryseq -o.

30 The sequences of SEQ ID NO: 78-81 were determined to have less than 50% identity to sequences in the SwissProt database using the computer algorithm BLASTP as described

above. The sequences of SEQ ID NO: 51, 53, 55, 56, 71, 83 and 88 were determined to have less than 75% identity to sequences in the SwissProt database using the computer algorithm BLASTP, as described above. The sequences of SEQ ID NO: 50, 52, 54, 57-68, 82 and 84-87 were determined to have less than 90% identity to sequences in the SwissProt 5 database using the computer algorithm BLASTP, as described above. Finally, the sequences of SEQ ID NO: 45-49, 69, 70 and 72-77 were determined to have less than 98% identity to sequences in the SwissProt database using the computer algorithm BLASTP, as described above.

10 BLASTX Polynucleotide Analysis

The isolated cDNA sequences were compared to sequences in the SwissProt protein database using the computer algorithm BLASTX. Comparisons of DNA sequences provided in SEQ ID NOS: 1-44, to sequences in the SwissProt DNA database (using BLASTX) were made as of April 28, 2003, using BLAST algorithm Version 2.0.11 [Jan-20-2000], and the 15 following Unix running command: blastall -p blastx -d swissprotdb -e 10 -FF -G0 -E0 -r 1 -v 30 -b 30 -i queryseq -o.

The sequences of SEQ ID NO: 27 and 34-37 were determined to have less than 50% identity, determined as described above, to sequences in the SwissProt database using the computer algorithm BLASTX, as described above. The sequences of SEQ ID NO: 3, 4, 6-20 19, 21-26, 28, 29, 33 and 38-44 were determined to have less than 75% identity, determined as described above, to sequences in the SwissProt database using the computer algorithm BLASTX, as described above. Finally, the sequences of SEQ ID NO: 1, 2, 5, 20 and 30-32 were determined to have less than 90% identity, determined as described above, to sequences in the SwissProt database using the computer algorithm BLASTX, as described above.

25

Figs. 3-41 show the positions of domains within the amino acid sequences of SEQ ID NO: 45-48, 53-70 and 72-88, respectively. These domains were determined with InterProScan software Release v3.1, November 6, 2001. The InterPro database integrates PROSITE, PRINTS, Pfam, ProDom, SMART and TIGRFAMs databases, and the addition of 30 others is scheduled. InterPro data is distributed in XML format and it is freely available under the InterPro Consortium copyright. The European Bioinformatics Institute (EBI) is a

non-profit academic organization that forms part of the European Molecular Biology Laboratory (EMBL): Wellcome Trust Genome Campus, Hinxton, Cambridge, CB10 1SD UK.

5

Example 2

USE OF CHALCONE SYNTHASE GENES TO MODIFY TANNIN BIOSYNTHESIS

10 Certain *Arabidopsis* mutants of the *transparent testa* (*tt*) phenotype do not make the anthocyanin pigment cyanidin and therefore have no seed coat color. The genes responsible for many of these mutants have now been identified as shown in Table 3.

TABLE 3

Enzyme	Abbreviation	Locus	Chromosome
Dihydroflavanol-4-reductase	DFR	<i>tt3</i>	5
Chalcone synthase	CHS	<i>tt4</i>	5
Chalcone isomerase	CHI	<i>tt5</i>	3
Flavanone 3-β-hydroxylase	F3βH	<i>tt6</i>	3

15

Over-expression of the maize gene for CHS has been shown to complement the *Arabidopsis tt4* mutant, thereby restoring cyanidin synthesis and seed coat color (Dong *et al.*, *Plant Physiol.* 127:46-57, 2001). Complementation of these *Arabidopsis* mutants may therefore be employed to demonstrate the function of the inventive polynucleotides encoding enzymes involved in the tannin biosynthetic pathway.

20 Two chalcone synthase genes were identified from *F. arundinacea* (SEQ ID NO: 32 and 33). Sense constructs containing a polynucleotide including the coding region of one chalcone synthase gene, FaCHS2, (SEQ ID NO: 33) under the control of the CaMV 35S promoter were inserted into a binary vector and used to transform *Agrobacterium tumefaciens* LBA4404 using published methods (*see*, An G, Ebert PR, Mitra A, Ha SB, "Binary Vectors," *in* Gelvin SB, Schilperoort RA, eds., *Plant Molecular Biology Manual*, Kluwer Academic Publishers: Dordrecht, 1988). The presence and integrity of the binary

vector in *A. tumefaciens* was verified by polymerase chain reaction (PCR) using the forward primer provided in SEQ ID NO: 89 and reverse primer provided in SEQ ID: 90.

The *A. tumefaciens* containing the sense gene construct were used to transform *Arabidopsis tt4* mutants by floral dipping (Clough and Bent, *Plant J.* 16:735-743, 1998) and several independent transformed plant lines were established for the sense. Transformed plants containing the appropriate tannin gene construct were verified using PCR.

The presence of cyanidin in the transformed plants is demonstrated by a phenotypic change in plant seedling color and by analyzing cyanidin extracts made from transgenic plants grown under stressed conditions (Dong *et al.*, *Plant Physiol.* 127:46-57, 2001).

Briefly, cyanidins are extracted from plant tissue with an acid/alcohol solution (HCl/methanol) and water. Chlorophyll is removed by freezing the extracts followed by centrifugation at 4 °C at 20,000 x g for 20 min. Any remaining chlorophyll is removed through a chloroform extraction. The absorbance at 530 nm is measured for each of the cyanidin extracts. Non-transgenic wild type and control *Arabidopsis* plants are used as controls.

Example 3

USE OF SUCROSE TRANSPORTERS TO COMPLEMENT A YEAST STRAIN

UNABLE TO GROW ON SUCROSE

Two *Lolium perenne* genes, LpSUT2 (SEQ ID: 25) and LpSUT-like (SEQ ID: 27), and two *Festuca arundinacea* genes, FaSUT1 (SEQ ID NO: 22) and FaSUT2 (SEQ ID NO: 26) share amino acid sequence identity with sucrose transporter (SUT1 and SUT2) genes from other plant species (Barker *et al.*, *Plant Cell* 12:1153-1164, 2000; Weise *et al.*, *Plant Cell* 12:1345-1355, 2000; Lemoine, *Biochim. Biophys. Acta* 1465:246-262, 2000). The first plant gene encoding a sucrose carrier protein, from spinach, was isolated by functional expression in a yeast strain, SUSY7 (Riesmeier *et al.*, *EMBO J.* 11:4705-4713, 1992).

The gene of SEQ ID NO: 27 was digested and cloned into the yeast expression vector pYEP 112 A1 NE for functional complementation using this yeast system. Plasmid DNA was verified by sequencing and transformed into *S. cerevisiae* strain SUSY7, which had been

engineered to express cytosolic sucrose synthase enabling it to metabolize sucrose entering the cell. Constitutive expression of the grass sucrose transporters within this yeast strain facilitated transport of sucrose in to the cell and its growth on sucrose minimal media. Growth rates of recombinant and wild type yeast strains in both sucrose and glucose minimal media were observed.

Results showed that the yeast strain containing the gene of SEQ ID NO: 27 was able to grow on sucrose minimal medium because the constitutive expression of the SUT-like gene within this yeast strain facilitated transport of sucrose into the cell.

10

Example 4

USE OF ALKALINE/NEUTRAL INVERTASES TO CLEAVE SUCROSE

A number of *Lolium perenne* and *Festuca arundinacea* genes (SEQ ID NO: 5, 7 and 9-14) were identified that share amino acid sequence identity with alkaline/neutral invertase genes from other plant species (Sturm *et al.*, *Physiol. Planta* 107:159-165, 1999; Gallagher and Pollock, *J. Exp. Bot.* 49:789-795, 1998).

L. perenne gene AN_INV8 (SEQ ID NO: 12) was amplified by PCR from the start methionine using forward (SEQ ID NO: 91) and reverse (SEQ ID NO: 92) primers, then cloned into the pET41a expression plasmid. The resulting plasmid was transformed into *E. coli* BL21 cells using standard protocols, and protein expression induced using IPTG. The soluble recombinant protein was assayed for its ability to cleave sucrose. Cells were lysed in citrate buffer and the soluble protein incubated with 50mM sucrose in citrate buffer pH7. Reactions were terminated by boiling. Cleavage of the sucrose by neutral invertase activity was determined by the formation of glucose in this reaction. Levels of glucose were determined with a Glucose HK assay kit GAHK-20 (Sigma, St Louis MO) utilizing hexokinase coupled to glucose-6-phosphate dehydrogenase, and reduction of NAD measured by absorbance at 340nm.

Fig. 1 shows the invertase activity of recombinant AN_INV8 protein, measured as the amount (in μ g) of glucose release from cleavage of sucrose per hour at pH7, and that of an empty vector (pET41a) control sample. The results showed that the purified protein released

35 µg of glucose per hour through the invertase cleavage of sucrose. No release was measured with the empty vector control.

Example 5

5 USE OF PYROPHOSPHATE-DEPENDENT PHOSPHOFRUCTOKINASE TO PHOSPHORYLATE
FRUCTOSE-6-PHOSPHATE

Two *Lolium perenne* genes, LpPFPA (SEQ ID: 15) and LpPFPB (SEQ ID NO: 18), and two *Festuca arundinacea* genes, FaPFPA (SEQ ID NO: 16) and FaPFPB (SEQ ID NO: 19) share amino acid sequence identity with the A and B subunits of pyrophosphate-dependent phosphofructokinase genes (PFP) from other plant species (Todd *et al.*, *Gene* 152:181-186, 1995; Carlisle *et al.*, *J. Biol. Chem.* 265:18366-18371, 1990).

The entire coding regions were cloned into expression vector pBK-CMV, under the control of the CMV promoter for expression of recombinant protein in mammalian cells. 15 The PFPA and PFPB genes from *Lolium perenne* or *Festuca arundinacea* were co-transfected in to mammalian HEK293T cells and protein extracted 48 hours later. Protein was also extracted from cells transfected with a negative control vector containing the β-galactosidase gene. Purified potato PFP (Sigma, St. Louis MO) was used as positive control. Activity of the PFP enzyme was measured spectrophotometrically by a decrease NADH and 20 absorbance at 340 nm in a coupled reaction as described previously (Theodorou and Kruger, *Planta* 213:147-157, 2001). Briefly, the conversion of fructose-6-phosphate to fructose-1,6-diphosphate in the presence of activator, fructose-2,6-diphosphate was initiated by the addition of pyrophosphate and measured in a coupled reaction with aldolase, triose phosphate isomerase and glycerophosphate dehydrogenase.

25 Fig. 2 shows the PFP activity of the purified protein (conversion of fructose-6-phosphate to fructose-1,6-diphosphate) measured as conversion of PPi to inorganic phosphate. No conversion was obtained with the β-galactosidase negative control.

Example 6USE OF SUCROSE PHOSPHATE SYNTHASE ENZYMES TO SYNTHESIZE SUCROSE

A *Lolium perenne* polynucleotide sequence (SEQ ID NO: 20) and a *F. arundinacea* polynucleotide sequence (SEQ ID NO: 21) have been identified that share identity with 5 sucrose phosphate synthase (SPS) from other plant species. These genes are expressed in *E. coli* or *Pichia* using standard protocols, and the resulting purified protein assayed for its ability to synthesize sucrose from fructose-6-phosphate and uridine 5'-diphosphoglucose. Sucrose is detected by adding NAD and UDP-Glucose dehydrogenase, followed by the addition of anthrone reagent and then measuring the change in absorbance at 620 nm (Botha 10 and Black, *Aust. J. Plant Physiol.* 27:81-85, 2000).

SEQ ID NOS: 1-88 are set out in the attached Sequence Listing. The codes for nucleotide sequences used in the attached Sequence Listing, including the symbol "n," conform to WIPO Standard ST.25 (1998), Appendix 2, Table 1.

15 All references cited herein, including patent references and non-patent publications, are hereby incorporated by reference in their entireties.

While in the foregoing specification this invention has been described in relation to certain preferred embodiments, and many details have been set forth for purposes of illustration, it will be apparent to those skilled in the art that the invention is susceptible to 20 additional embodiments and that certain of the details described herein may be varied considerably without departing from the basic principles of the invention.

Claims

We claim:

1. An isolated polynucleotide comprising a sequence selected from the group consisting of: SEQ ID NO: 1-44.
2. An isolated polynucleotide comprising a sequence selected from the group consisting of:
 - (a) complements of SEQ ID NO: 1-44;
 - (b) reverse complements of SEQ ID NO: 1-44;
 - (c) reverse sequences of SEQ ID NO: 1-44;
 - (d) sequences that are 100-mers of a sequence of SEQ ID NO: 1-44;
 - (e) sequences that are 40-mers of a sequence of SEQ ID NO: 1-44; and
 - (f) sequences that are 20-mers of a sequence of SEQ ID NO: 1-44.
3. An isolated polynucleotide comprising a sequence selected from the group consisting of:
 - (a) sequences having at least 75% identity to a sequence of SEQ ID NO: 1-44;
 - (b) sequences having at least 90% identity to a sequence of SEQ ID NO: 1-44;
 - (c) sequences having at least 95% identity to a sequence of SEQ ID NO: 1-44;
 - (d) sequences having at least 98% identity to a sequence of SEQ ID NO: 1-44; and
 - (e) sequences that hybridize to a sequence of SEQ ID NO: 1-44 under stringent hybridization conditions.
4. An isolated polypeptide encoded by a polynucleotide of any one of claims 1-3.
5. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of: SEQ ID NO: 45-88.

30

6. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:

- (a) sequences having at least 75% identity to a sequence of SEQ ID NO: 45-88;
- (b) sequences having at least 90% identity to a sequence of SEQ ID NO: 45-88;
5 and
- (c) sequences having at least 95% identity to a sequence of SEQ ID NO: 45-88.

7. An isolated polynucleotide that encodes a polypeptide of any one of claims 5 and 6.

10 8. An isolated oligonucleotide probe or primer comprising at least 10 contiguous residues complementary to 10 contiguous residues of a nucleotide sequence recited in any one of claims 1-3.

9. A kit comprising a plurality of oligonucleotide probes or primers of claim 8.

15 10. A genetic construct comprising a polynucleotide of any one of claims 1-3.

11. A transgenic cell comprising a genetic construct according to claim 10.

20 12. A genetic construct comprising, in the 5'-3' direction:

- (a) a gene promoter sequence;
- (b) a polynucleotide sequence comprising at least one of the following: (1) a polynucleotide coding for at least a functional portion of a polypeptide of any one of claims 5 and 6; and (2) a polynucleotide comprising a non-coding
25 region of a polynucleotide of any one of claims 1-3; and
- (c) a gene termination sequence.

13. The genetic construct of claim 12, wherein the polynucleotide sequence is in a sense orientation.

30

14. The genetic construct of claim 12, wherein the polynucleotide is in an anti-sense orientation.

15. A transgenic plant cell comprising a genetic construct of claim 12.

5

16. A plant comprising a transgenic plant cell according to claim 12, or fruit or seeds or progeny thereof.

17. The plant of claim 16, wherein the plant is selected from the group consisting of:

10 *Festuca arundinacea* and *Lolium perenne* species.

18. A method for modulating at least one of the fructan composition, cellulose, starch and tannin composition of a plant, comprising modulating the activity of a polypeptide of any one of claims 5 and 6 in the plant.

15

19. A method for modulating at least one of the fructan composition, cellulose composition, starch composition and tannin composition of a plant, comprising modulating the activity of a polynucleotide of any one of claims 1-3 in the plant.

20

20. The method of claim 19, comprising stably incorporating into the genome of the plant a polynucleotide of any one of claims 1-3.

21. The method of claim 19, comprising stably incorporating into the genome of the plant a genetic construct of any one of claims 10 and 12.

25

22. A method for producing a plant having at least one of altered fructan composition, altered cellulose composition, altered starch composition and altered tannin composition, comprising:

30

(a) transforming a plant cell with a genetic construct of any one of claims 10 and 12 to provide a transgenic cell; and

(b) cultivating the transgenic cell under conditions conducive to regeneration and mature plant growth.

23. A method for modifying the activity of a polypeptide involved in a fructan, cellulose, 5 starch or tannin biosynthetic pathway in a plant, comprising modulating the activity of a polynucleotide of any one of claims 1-3 in the plant.

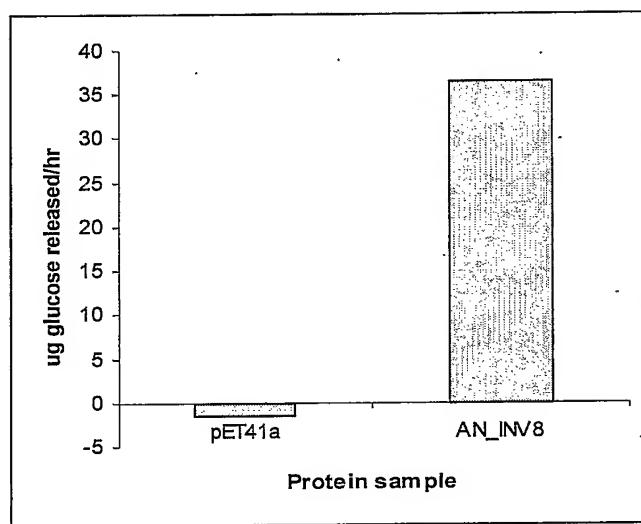
24. The method of claim 23, comprising stably incorporating into the genome of the plant a genetic construct of claim 12.

10

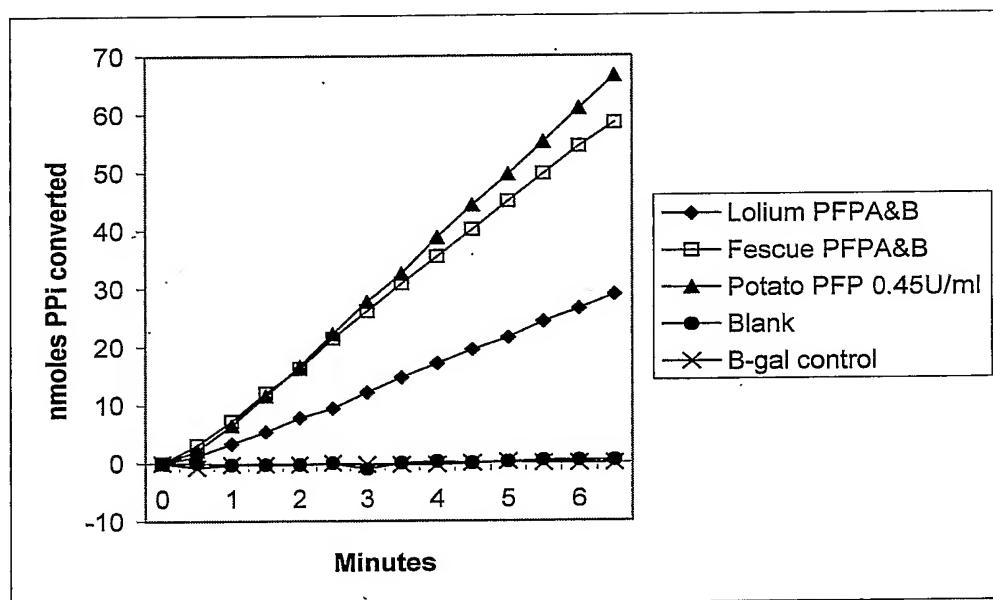
25. A method for modifying the activity of a polypeptide involved in a fructan, cellulose, starch or tannin biosynthetic pathway in a plant, comprising introducing into cells of the plant double stranded RNA corresponding to a polynucleotide of any one of claims 1-3, thereby inhibiting expression of a polypeptide encoded by the polynucleotide.

15

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Fig. 1

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Fig. 2

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Fig. 3

MAAAAVAPDAKIEKFRDAVAKLGEISENEKAGCISLVSRYLSGEAEQIEWSKIQTPTDEVVVPYDTLAPAP
EDLDAMKALLDKLVVLKLNGGLGTTMGCTGPKSVIEVRNGFTFLDLIVIQIESLNKKYGCDVPLLLMNSFN
THDDTQKIVEKYSNSNINIHTFNQSQYPRIVTEDFLPLPSKGQSGKDGWYPPGHGDVFPSLNNSGKLDTLL
SQKEYVFVANSNDLGAIVDIKILNHLINNKNEYCMEVTPTKTLADVKGGTLISYEGRVQLLEIAQVPDEHV
 NEFKSIEKFKIFNTNNLWVNLAIAKRLVEADALKMEIIPNPKEVDGVKVLQLETAAGAAIRFFDNAIGING
 PRSRFLPVKATS DLLVQSDLYTLVDGYVIRNPARVKPSNPSIELGPEFKKVASFLARFKSIPSIVELDSL
 KVSGDVSFGSGIVLKGNVTIAAKSGVKLEIPDGAVLENKDINGPEDL

Fig. 4

MAAVAADAKIEKFRDAVAKLDEISENEKAGCISLVSRYLSGEAEQIEWSKIQTPTDEVVVPYDTLAPAPQD
LDAMKALLDKLVVLKLNGGLGTTMGCTGPKSVIEVRNGFTFLDLIVIQIESLNKKYGCDVPLLLMNSFNTH
DDTQKIVEKYSNSNINIHTFNQSQYPRIVTEDFLPLPSKGQSGKDGWYPPGHGDVFPSLNNSGKLDTLLSQ
GKEYVFVANSNDLGAIVDIKILNHLINNQNEYCMEVTPTKTLADVKGGTLISYEGRVQLLEIAQVPDEHVNE
 FKSIEKFKIFNTNNLWVNLAIAKRLVEADALKMEIIPNPKEVDGVKVLQLETAAGAAIRFFKAIGINGPR
 SRFLPVKATS DLLVQSDLYTLVDGYVIRNPARVKPSNPSIELGPEFKKVASFLARFKSIPSIVELDSLKV
 SGDVTFGSGVVLKGNVTIAAKSGVKLEIPDGAVLENKDINGPEDL

Fig. 5

CLRRRTYSNSGDTHADPNGPVYYGGWYHLYQHNPyGDSWGNVSGHAvSKDLVNWRHLPVALVPDOWYDI
NGVLGSITVLPDGRVILLYTGNTDFSQVQCLAVPADPSDPLLRSWIKHPANPILFPPPGIGLKDFRDPL
 TAWFEHSNTWRTIIGSKDDDHAGITVLSYKTTDFVNYELMPGNMHRGPDTGMYECLDIYPVGGNSSEML
GGDSSPEVLFVLKESANDEWHYALGWFDATANTWTPQDPEADLGIGLRYDWGKYYASKSFYDPIKNRRV
 VWAFFGETDSEQADAKGWAISMSIPRMVELDKKTRTNLIQWPVEEETLRRNVTDLGGITVEAGSVIHL
 LOQGGOLDIEASFRLNSSIDALNEADVGFNCSSAGAAVRGALGPFGLLVFADGRHEQTAAYFYVSKGLD
GSLLTHYCHDESRSTRAKDVVSRVVGGTVPLDGETFSVRVLVDHSIVQSFVMGGRTTVTSRAYPTEAIYA
 AAGVYLFNNATSATITAEGLVVYEMASAESQAFLADDM

Fig. 6

MESSAVVVPGTAPLLPYDSRENQSSGGVWWRAACAASAVVLLVVVGGFFAGGRVDLGQAGEVSATSSVPAA
 MMEIPRSRGKNFGVSEKADGGFPWSNAMLOWQHTGFHQPLKHYMDPNGPVYYGGWYHLYQHNPyGDSW
 GNVSGHAvSKDLVNWRHLPVALVPDOWDINGVLTGSITVLPDGRVILLYTGNTDFSQVQCLAVPADPS
 DPPLLRSWIKHPANPILFPPPGIGLKDFRDPLTAWFEHSNTWRTIIGSKDDDHAGITVLSYKTTDFVNYEL
 MPGNMHRGPDTGMYECLDIYPVGGNSSEMLGGDSSPEVLFVLKESANDEWHYALGWFDATANTWTPQD
 PEADLGIGLRYDWGKYYASKSFYDPIKNRRVWAFGETDSEQADAKGWAISMSIPRMVELDKKTRTNLI
 QWPVEEETLRRNVTDLGGITVEAGSVIHLPLQQGQLDIEASFRLNSSIDALNEADVGFNCSSAGAAV
 RGALGPFGLLVFADGRHEQTAAYFYVSKGLDGSILLTHYCHDESRSTRAKDVVSRVVGGTVPLDGETFSVR
 VLVDHSIVQSFVMGGRTTVTSRAYPTEAIYAAGVYLFNNATSATITAEGLVVYEMASAESQAFLADDM

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Fig. 7

MAIAAAAALLPLHLGCSDAAPRRPGNSLRAHLRKGGIRGRRSPPCAVNSLHPSGNPKTPGGGDVGGAWGL
NGGATAKPDHAPPSSQRRRAPRVDVEEEAWALLRESVSYCGSPVGTIAACDPNDASPLNYDQVFIRDFVPSG
VAFLLKGEHEIVRNFIHLTLQLQSWEKTIDCHSPGQGLMPASFKVRVPLDGGDDGATEEVLDPDFGEAAI
GRVAPVDSLWIIILLRAYGKCGDLSFHERDVQVTGIKLILKLCLADGFDMPTLLVTDGSCMMDRRMGI
HGHPLEIQALFYSALLSAREMLTPEDGSADLIRALNSRLMALSFHIREYYWLEKRKLNEIYRYKTEEYSYD
AVNKFNIYPDQIPPWLVWIPPKGGYFIGNLQPAHMDFRFFSLGNLWSIVSSLATADQSHAILDLVEAKWS
DLVAEMPMKICYPALEDQEWKFITGSDPKNTPWSYHNGGSWPTEQWLTVCIAKMRPEIAARAVEVAESR
IISMDKWPEYYDTKRGFIGKQARLFQTWSIAGFLVAKLLENPEKSRLWNNEDEEILNALSLMTGPSSPK
RKRGKTYIV

Fig. 8

MNGQTTMGLAAAAAAAVRPCRRRLLSSASAAAAAKASATPLFPRCSHPQHQHQSRRIPFLVSAASHTSQSD
PSTTPTPVTS DPRSAVAGNLPFFDRVLFGSFPLETPVVEEPAPAPPADAQASASPVREESDTEREAWL
LRRAVVSYCGDPVGTVAEADPECTEMLNYDQVFIRDFVPSALAFLMRGETEIVRNFLHLLTQLQSWEKTV
CYSPGQGLMPASEFKITVPLDENNEAEEVLDPDFGESAI GRVAPVDSLWIIILLRAYCKFTGDYSLQER
VDVQTGIKLILSICLTDGFDMPTLLVTDGSCMIDRRMGIHGHPLEIQALFYSALRCSEMI VMNDGSKHL
LQAINNRLSALSFHIREEYYWVDMKKINEIYRYKTEEYSHDATNKFNIIYPEQIPSWLVDWVPEKGGYLIGNL
QPAHMDFRFFSLGNLWAISSSLTPTQAEGILSILEEKWDDL VANMPLKICY PAMEDDEWRIVTGSDPKNT
PWSYHNGGSWPTEQWLTACIKMGRPELARRAIAVAEIKISADKWPEYYDTRSGRFVGKQSR SYQTWTIA
GFLTSKILLENPelasiltCDEDLELEGCACLSKRTCSRRVTKSDIIIG

Fig. 9

MAIAAAAALLPLHLGCSDAAPRRPGNSLRAHLRKGGIRGRRSPPCAVNSLHPSGNPKTPGGGDVGGRGV
NGGATAKPDHAPPSSQRRRAPRVDVEEEAWALLRESVSYCGSPVGTIAACDPNDASPLNYDQVFIRDFVPSG
VAFLLKGEHEIVRNFIHLTLQLQSWEKTIDCHSPGQGLMPASFKVRVPLDGGDDGATEEVLDPDFGEAAI
GRVAPVDSLWIIILLRAYGKCGDLSFHERDVQVTGIKLILKLCLADGFDMPTLLVTDGSCMMDRRMGI
HGHPLEIQALFYSALLSAREMLTPEDGSADLIRALNSRLMALSFHIREYYWLEKRKLNEIYRYKTEEYSYD
AVNKFNIYPDQIPPWLVWIPPKGGYFIGNLQPAHMDFRFFSLGNLWSIVSSLATADQSHAILDLVEAKWS
DLVAEMPMKICYPALEDQEWKFITGSDPKNTPWSYHNGGSWPTEQWLTVCIAKMRPEIAARAVEVAESR
IISTDKWPEYYDTKRGFIGKQARLFQTWSIAGFLVAKLLENPEKSRLWNNEDEEILNALSLMTGPSSPK
RKRGKTYIV

Fig. 10

MKRVSSHVIASEAEINLDLSRLLIDKPRYTLEKRKFDEQSWSLTHTHRQNDGFDSDLQSPAERTGFDS
PFSMGTHFGEPSGPHPLVNEAWEALRKSVVYFRGQPVGTIAAVDHASEEVLYDQVFVRDFVPSALAFIMN
NEPEIVKNFLLKTLHQLQSSEKMDRFLKGAGAMPAFKVDRNKSNTETLVADFGEAI GRVAPVDSLGFWW
TILLRAYTKYTDGASLSESPDCQKCMRLILNLCLSEGFDFTPTLLCTDGSCMIDRRMGIYGYPIEIQALFY
MALRCALQMLKPDGEGKDFTEKIGQRLHALTYHMRNYFWLDFPHLNNIYRYKTEEYSHAVNKFNVIPDSI
PDWVFDMPMPCRGGYFLGNVSPAMMDFRWFALGN CIAIISSLATPEQSSAIDLIEERWDELVGEVPLKICY
PAIENHEWRIITGCDPKNTRWSYHNGGSWPVLLWLLTAACIKTGRPQMAKRAIELSEARLLKDGWPEYYDG
KLGKFVKGQARKFQTWSIAGYLVARMMLEDPSTLMMISMEEDRPVKPTMRRSASWNA

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Fig. 11

MEAPGGGAGPMPTPSHASIADSDDFDLSRLLNHRPRINVERQRSFDDRSLSGLYLSAMDSRGGYMDSYD
 MYSPGGGLRSLTGTGTPASSRLSFEPOQLVAEAEALRRSLVCFRGEPLGTIAAVDSSDEVLNYDQVFVRD
 FVPSALAFLMNGEPDIVKNFLKTLQGWEKRIDRFKLGEAMPASFKVLKDPKRGVDTLAADFGESAIG
 RVAPADSGFWIILLRAYTKSTGDLTAAETPECQKGIRLIMNQCLAEGFDTFPTLLCADGCCMIIDRRMGVY
 GYPIEQALFFMSLRCALLLKPAVEGNSSKDDIMERIVTRLHALSYHMRSYFWLDFQQLNVIIYRFKTE
 EYSHTAVNKFNVIPESIPDWLFDFMPSRGGYFVGNVSPARMDFRWALGNCAILASLATPEQAGAIMDLI
 EERWEDLIGEMPLKICYPTIEGHEDWQNVTGCDPKNTRWSYHNGGSWPVLIWLLTAACIKTGRLKIARRAID
 LAEARLGKDGPWEYYDGKLGKQARKHQTWSIAGYLVAKMLEDPSHGLGMIS

Fig. 12

MEFGAPGGMRRSASHNSLSGSDDFDLTHLLNKPRINVERQRSFDDRSLSDVSYSGGGHARGAGGGFDGMYS
 PGGGLRSLVGTPASSALHSFEPHPIVGDWEALRRSLVFRGQPLGTIAAYDHASEEVLYDQVFVRDFVP
 SAMAFLMNGEPEIVKNFLKTLLQGWEKKVDRFKLGEAMPASFKVLHDDKKGVDTLHADFGESAIGRVA
 PVDSGFWIILLRAYTKSTGDLTAAETPECQKAMRLLILSCLSEGFDTFPTLLCADGCCMIIDRRMGVYGP
 IEIQSLFFMALRCALLMLKHDNEGKDVERIATRLHALSYHMRSYFWLDFQQLNDIYRYKTEEYSHTAVNK
 FNVIPDSIPDWLFDFMPCEGGFFVGNVSPARMDFRWALGNMIAIVSIATPEOSTAIMDIEERWEEILIG
 EMPLKICPAIENHEWRIVTGCDPKNTRWSYHNGGSWPVLIWLLTAASIKTGRPQIARRAIDLAEERRLLKD
 GWPEYYDGKLGKQARKFQTWSIAGYLVAKMLEDPSHGLGMIALEEDKAMKPVLRRSASWTN

Fig. 13

MDSDYGVPRELSEVQKKRTLYQPDLPCLQGTTVVRVEYGDVAIAADPAGAHVI SHAFPHYGQPLAHFLRK
 AANVADAKVISEHPAVRVGIVFCGRQSPGGHNVIWGLHDAIKAHNPNSKLIGFLGGSDGLLAOKTLEITDE
VLSSYKNQGGYDMLGRTKDQIRTTEQVNGAMASCQALKLDALIIIGGTSNTDAQLAETFAEKCATKV
 GVPVTLNQFDLKNQFVETTVGFDTICKVNSQLISNMCTDALSAEKYYYFIRMMGRKASHVALECALOSHPNM
 VILGEEVAASKLTIFDITKQICDAVQARAEKDNHGVLIPEGLVESIPELYALLQEINGLHGKGVSIE
NSQLSPWASALFFLPQFIRQQLLRPESDDSAQLSQIETEKLLAQLVETEMNKRLKEGYKGKFNAICH
 FFGYQARGAMPSKFDCDYAYVLGHVSYHILAAGLNGYMATVNLKSPLNWKRCGAAPISSMMTVKRWSRG
 STTQIGKPAVHMASVDLRGKAYELLRQNSSCLEDIYRNPGPLQFEGPGSDSKPISLCVEDQDYMGRIKK
 LQEYLEKVKSVKPGCSQDVLKAALSAMSSVTDTLAIMTSSSTGQAPL

Fig. 14

MDSDYGVPRELSEVQKKRTLYQPELPPCCLQGTTVVRVEYGDVAIAADPAGAHVI SHAFPHYGQPLAHFLRK
 AANVADAKVISEHPAVRVGIVFCGRQSPGGHNVIWGLHDAIKAHNSNSKLIGFLGGSDGLLAOKTLEITDE
VLSSYKNQGGYDMLGRTKDQIRTTEQVNGAMASCQDLKLDALIIIGGTSNTDAQLAETFAEKCATKV
 GVPVTLNQFDLKNQFVETTVGFDTICKVNSQLISNMCTDALSAEKYYYFIRMMGRKASHVALECALOSHPNM
 VILGEEVAASKLTIFDITKQICDAVQARAEKDNHGVLIPEGLVESIPELYALLQEINGLHGKGVSIE
NSQLSPWASALFFLPQFIRQQLLRPESDDSAQLSQIETEKLLAQLVETEMNKRLKEGYKGKFNAICH
 FFGYQARGAMPSKFDCDYAYVLGHVSYHILAAGLNGYMATVNLKSPLNWKRCGAAPISSMMTVKRWSRG
 STTQIGKPAVHMAVDLRGKAYELLRQNSSCLEDIYRNPGPLQFEGPGSDSKPISLCVEDQDYMGRIKK
 LQEYLEKVKSVKPGCSQDVLKAALSAMSSVTDTLAIMTSSSTGQAPL

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Fig. 15

MAAAAVATSNGASANGPTPGRLASVYSEVQTSRIAHALPLPSVLRSHFTLADGAASSATGNPEEIAKLFPN
 LYGQPSAAVPSAQPVATKPLKIGVVLSGGQAPGGHNVICGIFDYLOERAKGSTMGYFKGGPAGVMKGKYV
ELNADFVPYRNOGGFDMICSGRDKIETPEQFKOAEDTVTKLDLGLVVIGGDSNTNACLGEYFRGRNL
KTRVIGCPKTIDGDLKCKEVPTSFGFDTACKIYSEMIGNVMTDARSTGKYYHFVRLMGRASHITLECALO
THPNVSLIGEEVAEKKETLKQVTDYITDVICRAEGNYGVVILPEGLIDFIPEVOKLIENEILAHDV
VDEAGAWKSKLQPERQLFDLPNTIQEQLLRDPHGNVQVAKIETKMLIAMVETELEKRRSAGKYS
FRGQSHFFGYEGRCGLPTNFDSSCYALGYGAGALLQFGKTGLISSVGNLAPVEEWTVGGTPLTAMDV
RRHGKFKPVIKKAMVELDAPFKKFASMRDEWAIKNRYISPGPIQFSGPGDASNHTLMLEGAQT

Fig. 16

MAAAAVATSNGASANGPTPGRLASVYSEVQTSRIAHALPLPSVLRSHFTLADGAASSATGNPEEIAKLFPN
 LYGQPSAAVPSAQPVATKPLKIGVVLSGGQAPGGHNVICGIFDYLOERAKGSTMGYFKGGPAGVMKGKYV
ELNADFVPYRNOGGFDMICSGRDKIETPEQFKOAEDTVNKLDLGLVVIGGDSNTNACLGEYFRGRNL
KTRVIGCPKTIDGDLKCKEVPTSFGFDTACKIYSEMIGNVMTDARSTGKYYHFVRLMGRASHITLECALO
THPNVSLIGEEVAEKKETLKQVTDYITDVICRAEGNYGVVILPEGLIDFIPEVOKLIENEILAHDV
VDEAGAWKSKLQPERQLFDLPNTIQEQLLRDPHGNVQVAKIETKMLIAMVETELEKRRSAGKYS
FRGQSHFFGYEGRCGLPTNFDSSCYALGYGAGALLQFGKTGLISSVGNLAPVEEWTVGGTPLTAMDV
RRHGKFKPVIKKAMVELDAPFKKFASMRDEWAIKNRYISPGPIQFSGPGDASNHTLMLEGAQT

Fig. 17

MAAAAVATSNGASANGPTPGRLASVYSEVQTSRIAHALPLPSVLRSNFTLADGPASSATGNPEEIAKLFPN
 LYGQPSAAVPSAEPVPTKPLKIGVVLSGGQAPGGHNVICGIFDYLOERAKGSTMGYFKGGPAGIMKGKYI
ELNADFVPYRNOGGFDMICSGRDKIETPEQFKOAEDTVNKLDLGLVVIGGDSNTNACLGEYFRGRNL
KTRVIGCPKTIDGDLKCKEVPTSFGFDTACKIYSEMIGNVMTDARSTGKYYHFVRLMGRASHITLECALO
THPNVSLIGEEVAEKKETLKQVTDYITDVICRAEGNYGVVILPEGLIDFIPEVOKLIENEILAHDV
VDEAGAWKSKLQPERQLFDLPNTIQEQLLRDPHGNVQVAKIETKMLIAMVETELEKRRSAGKYS
FRGQSHFFGYEGRCGLPTNFDSSCYALGYGAGALLQFGKTGLISSVGNLAPVEEWTVGGTPLTAMDV
RRHGKFKPVIKKAMVELDAPFKKFASMRDEWAIKNRYISPGPIQFSGPGDASNHTLMLEGAQT

Fig. 18

MVGNDNWINSYLDAILDAGKSSIGGDRPSLLLTERGHFSARYFVEEVITGYDETDLYKTWLTRANAMRSPO
 ERNTRLENMTWRIWNLARKKELEKEACRLLKRHPETEKRTDATAADMSEDLFGEKGEDAGDPGVAYGD
STGSPKTSVDKLIVLISLHGLVRENMELGRDSTGQVKVVEFAKALSSPGVYRVDLLTRQIV
PNFDRSYGEPEMLVSTTFKNSKHERGVNSGYIIRIPFGPKDKYLAEHMWPFIQDFVDGALSHIRMSK
TIGEICGHPVWPAVHGYASAGVAALSGALNPMAFTGHFLGKDKYLKQGRSQEINMTKI
KRIEEAEELSDAEVIASIATROEIEEQEQLLRDPHGNVQVAKIETKMLIAMVETELEKRRSAGKYS
GGEILRKYLVKWATSVVERKRERQMIFEDSEHSSTCAFKVVNPNHLPPKELRKLMRIQSLRCNA
NHSATRLSVTPIHASRSQAIRLFIRWGELPNVLGESGDSDYELGGLHRTIILKGDFNIANRH
TVRRYPLQDVVALDSNIIEVEGCTDVIKSALRQIGVPTQ

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Fig. 19

MVGGMCNDNWINSYLDAILDAGKGAPGGGAGPGGGRGGGGGAGDRPSLLLRERGHFSARRYFVEEVITG
 YDETDLYKTWSRANAMRSQERNTRLENMTWRIWNLARKKEXEAEEANRLLKRLETEKPRTDAAAEMSE
 DLFEQKGEDAGDASVAYGDSSASNTPRISIDKLYIVLISLHGLVRGENMELGRDSDTSGQVKYVVELAK
 ALSSCPGVYRVDLLTRQILAPNYDRGYGEPESETLLPTNLKNFHERGENSGAYITRIPFGPKDKYLAKEQL
 WPYVQEFDGALSHIVRMSKTIGEEICGHGPMWPAIIGHYASAGVAALLSGALNVHMLFTGHFFGRDKL
 EGLLKQGKOTREEINMTYKIMRRIEAEELSDASEIVIASTRQEIEEQWNLYDGFEVMLARKLRARVKRGA
 NCYGRYMPMRVIIPPGVEFGHMIQDFDMGEEDSPSPASEDPPPISEIMRFFTNPBKPLILAVARPYPEKN
ITTLVRAFGECRPLRELANLTIMGNEAISKMSNSMSAAVLTSVLTLEDYDLYGQVAPKHHKHSEVLDI
YRLAARTKGAFVNAYFEQFGVTLIEAMHGLPVIATKNGAPVEIHQVLNNGLLVDPHDQNAIADALYKLL
SEKOLWSRCRENGLKNIHQFSWPEHCKNYSRILTSRYPAPAFASNDQIKAPIKGRKYIIVIAVDSASKK
DLAFIIRNSIEATRTETSSGSTGFVLTSLTISEIHSLLISAGMVPTDFDAFICNSGSDLFYPQTGDSPS
TSRVTALDRNYQSRVEYHWGGEGLRKYLKVWASSVERGRMEKQVIFDDSEHSTCCLAFRVVNPNYLP
PLKELQKLMRVQSLRCHALYNHSATRLSVIPIHASRSQAIRYLSVRWGIELPNVILVGESGDSDYELFG
GLHKTVVNLGEFNTPANRIHTVRRYPLQDVIALDCSNIVGVQGCSTDCMRSTLEKLGIPTK

Fig. 20

MVRGGGNSEVELSVGAGGGGGGAGGLVEPPVPISLGRVLVAGMVAGGVQYGWALQLSLLTPYVQTLGLSHA
LTSFMWLCPPIAGLVVQPCVGLYSDKCTS RWGR RRFMTGCVLICIAVVIVGFSA DICAALGDSKEEC
YHGPRWHAAIVYVLFGLWLDFSNNTVQGPARALMADLSGKYGPSAANSIFCSWMALGNILGYSSGSTDKWH
KWF PFLRTRACCEACANLKGAFLVAVLFLCFCLVITLIFAKEVPYKRIAPLPTKANGQVEVEPSGPLAVFO
GIRNLPSGMP SVL LVTGLTWL SWFPFILYD TDWMGREIYHGDPKGTPAEMS AFQDGVRAGAFGLLINSII
GFSSFLIEPMCKRLGPRVVVVS SNFLVCIAM AATAIISWWSTKEFHEYVQHAITASKDIKIVCMALFAFLG
VPLA ILLSVPFAVTAQLAASKGGGQGLCTGVLNISIVIPOVIIALGAGPWDQ LGKGNIPAFAAAASFALI
GGIVGIFLLPKISRRSFRAVSTGGH

Fig. 21

ICVAVVVVGFSA DICAALGDSKEECSLYHGPRWHAAIVYVLFGLWLDFSNNTVQGPARALMADLSGKYGPS
AANSIFCSWMALGNILGYSSGSTDKWHKWFPLRTRACCEACANLKGAFLVAVLFLCFCLVITLIFAKEVP
YKRIAPLPTKANGQVEVEPSGPLAVFOQFRNLPSGMP SVL LVTGLTWL SWFPFILYD TDWMGREIYHGDPK
GTPAEASAFQDGVRAGAFGLLINSII GFSSFLIEPMCKRLGPRVVVVS SNFLVCIAM AATAIISWWSTKE
FHEYVQHAITASKDIKIVCMVLFAFLGVPLA ILLSVPFAVTAQLAANKGGGQGLCTGVLNISIVIPOVIIA
LGAGPWDQ LGKGNIPAFAAAASFALI
GGIVGIFLLPKISRRSFRAVSTGGH

Fig. 22

MVRGGGNSEVELSVGAGGGGGGAGGLVEPPVPISLGRVLVAGMVAGGVQYGWALQLSLLTPYVQTLGLSHA
LTSFMWLCPPIAGLVVQPCVGLYSDKCTS RWGR RRFMTGCVLICIAVVIVGFSA DICAALGDSKEEC
YHGPRWHAAIVYVLFGLWLDFSNNTVQGPARALMADLSGKYGPSAANSIFCSWMALGNILGYSSGSTDKWH
KWF PFLRTRACCEACANLKGAFLVAVLFLCFCLVITLIFAKEVPYKRIAPLPTKANGQVEVEPSGPLAVFO
GFRNLPSGMP SVL LVTGLTWL SWFPFILYD TDWMGREIYHGDPKGTPAEMS AFQDGVRAGAFGLLINSII
GFSSFLIEPMCKRLGPRVVVVS SNFLVCIAM AATAIISWWSTKEFHEYVQHAITASKDIKIVCMVLFAFLG
VPLA ILLSVPFAVTAQLAANKGGGQGLCTGVLNISIVIPOVIIALGAGPWDQ LGKGNIPAFAAAASFALI
GGIVGIFLLPKISRRSFRAVSTGGH

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Fig. 23

MPPPRRPTTGGTTTSAALPPPRKVPLRSLLRAASVACGVQFGWALQLSLLTPYVQELGIPHAFAISLVWL
GPISGLIVQPLIGHLSDRIAPADSPLGRRRPFIAAGAASIAFSVLTVGFSADLGRLFGDNVRPGSTRYGAI
IVYMIGFWLLDVGNNATQGPCRAFLADLTENDPRRTRIANAYFSLFMALGNILGYATGAY SGWYKIFPFTI
TE SCGVSCANLKSAFLLDIIIILAITYVTVVTVQDNPTFGSDEAAPRPSHEEAFLFELFGSFKYFTMPV
WMVLIVTSLTWIGWPFILFDTDWMGREIYRGSPE IVADTQKYHDGVRMGSFGIMLNSVLLGITSVVTEKL
CRKGAGLVWGVSNIMACFVAMLITYVAQNLDYGPSGAPTGIVVASLTVFTLGAPLSITYSIPYAM
ATSRVENLGLGQGLAMGILNLSIVPOIIVSLGSGPWDSLFGGNAPSFWVAAAASFIGGLVAILGLPRAR
IAPKKRSQR

Fig. 24

MPPPRRPNAGGTTSAPLPPPRKVPLRSLLRAASVACGVQFGWALQLSLLTPYVQELGIPHAFAISLVWLCGP
LSGLLVQPLIGHLSDRIAPADSPLGRRRPFIAAGAASIAFSVLTVGFSADLGRLFGDNIRPGSTRFGAII
YMIGFWLLDVGNNATQGPCRAFLADLTENDPRRTRIANAYFSLFMALGNILGYATGAY SGWYKIFPFTI
SCGVSCANLKSAFLLDIIIILAITYVTVVTVQDNPTFGSDEAAPRPSHEEAFLFELFGSFKYFTLPVWM
VLIVTSLTWIGWPFILFDTDWMGREIYRGSPE IVADTQKYHDGVRMGSFGIMLNSVLLGITSVVMEKL
CRKGAGLVWGVSNIMACFVAMLITYVAKNLDYGPSGAPTGIVVASLAVFTLGAPLSITYSIPYAMAT
SRVENLGLGQGLAMGILNLSIVPOIIVSLGSGPWDSLFGGNAPSFWVAAAASFIGGLVAILGLPRARIA
PKKRSQR

Fig. 25

MVDQDHGRRRQEETAVAAASSVPLLEKKPGDVYYVEGCPGCAVDRRKATDPGIPYGSEIYIWVVLCTA
IPISSILFPFLYFMIRDLHIAERTEDIGFYAGFVGAAFMFCRCLTSTIWGIAADRIGRKPVVIFGVFSVVI
NALFGLSVTYWMAIATRFLLLGALNGLGPMKAYATEVCRPEHEAALSLVSTAWGIGLIIGPAGGYLALP
AEKYPNIFSPDSILFGRFPYFLPCLCTSVFAAAVLIGCIWMPETLHKHKVNENRNQSVELEAHLIDPKEKV
EQSNSPDTKKSLFKNWPLMSSIIVYCVFSFHDMAYTEVFSLWAESDRTYGGSISEDVGQTLAITGSLL
VYQLFLYPRINRVLGPIKSSOIAAGCICIPILFAYPYMTLSEPGLSIVLNIASVKNNLGVTIITGTFIQ
NNAPQDQRGAANGLAMTGMSFFKAVAPAGAGIVFSWAQKRQHAFFPGDQMVFLLNIELLGLLTFK
FLAVPDKSDSN

Fig. 26

MSSMQFSSVLPLEGKACVCPVRSANNGCERLKVGDS~~SS~~LRHEMALRRKCNGARGGAADGAQCVLTSASP
DTLVVRSSFRMNYADPNEVAAVILGGGTGTOLFPLTSTRATPAVPIGGCYRLIDIPMSNCFNSGINKIFV
TQFNSASLNRHIHRTYLGGGINFTDGSVEVLATQMGEAGWFRGTADAVRKFIWVLEDYYKHKSIEHIL
ILSGDQLYRMDYMELVQKHVDDNADITLSCAPVGESRASYGLVKFDSSGRVIQFSEKPKGADLEAMKVD
SFLNFAIDDPAKNPYIASMGVYVFKREVLINLIKSRYTELHDFGSEILPRALHDNVQAYVFTDYWEDIG
IRSFFDANMALCEQPPKFEFDPKTPFFTSPRYLPPTKSDKRIKEAIISHGCFLRECTIEHSIIGVRSRL
NSGSVLKNAMMMGADLYETEDEISGLLSEGKVPIGVENSKLSNCIIDMNARIGRDVVIANSEGVQEADRP
EEGYIRSGIVVILKNATVKDGTVV

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Fig. 27

MSSMQFSSVLPLEGKACVCPVRSANNGCERLKVGDSSSLRHEMALRRKCNARGGAAADGAQCVLTSASP
 DTLVVRSFRMNYADPNEVAAVILGGGTGTOLFPLTSTRATPAVPIGCCYRLIDIPMSNCNSGINKIFVM
 TQFNSASLNRHIIHTYLGGINFTDGSVLAAQMPGEAAGWFRGTA~~DAVRKF~~WLEDYYKHKSIEHIL
 ILSGDQLYRMDYMELVQKHDDNADITLSCAPVGE~~SRASEYGLVKFDSSGRV~~IQFSEKPKGADLEAMKVDT
 SFLNFAIDDPAKNPYIA~~SMGVVF~~KREVILLNLKSRYTELHDFGSEILPRALHDHNQAYVFTDYWEDIGT
 IRSFFDANMALCEQPPKFEFYDPKTPFTSPRYPPTKSDCRIKEAIISHGCFRECTIEHSIIGVRSRL
 NSGSVILKNAMMMGADLYETEDEISGLLSEGKVPIVGGENSKLSNCIIDMNARI~~GRDVVIAN~~SEGVQEADRP
 EEGYYIRSGIVVILKNATVKDGTVV

Fig. 28

MTGAPPSTVMAMGAATSPCKILSATQR~~A~~AAASTSRESVSLRAPRGRQRPRGLALSAPARRPV
 FSPRAVSDSKSSQTCL~~D~~P~~A~~STSVLGI~~L~~GGGAGTR~~L~~YPLTKKRAKPAVPLGAN~~Y~~RLIDIPVSNC~~I~~NSNIS
 KIYVL~~T~~QFNSASLNRHLSRAYGSNIGGYKNEG~~F~~V~~E~~LAQQSPDNPNWFQGTADA~~V~~RQYLWL~~F~~EEHN~~V~~MEY
 IL~~A~~GDHLYRMDYEKF~~I~~QAHRET~~D~~ADITVAALPMDEERATAFGLMKIDE~~E~~GRIVEFAEKPKGEQLKAMMVDT
 TT~~I~~LG~~L~~D~~D~~VRAKEM~~P~~YIAS~~M~~GIYV~~I~~SKHV~~M~~QLRDQ~~F~~PGANDFGSE~~V~~PGATSTGMRVQAYLYDGYWEDI
 GTIEAFYNANLGITKKP~~I~~PDFSYDR~~S~~APIYTQPRHLPPSKVLDADVTDSV~~I~~GEGCVIKNC~~I~~HHSV~~V~~GLR
 SCISEGAI~~I~~EDTLLMGADYYETEADKLLADKG~~G~~PI~~I~~GIGKNSHIRRAI~~I~~DKNARIGDNV~~K~~IINV~~D~~NVQEA
 ARETDGYFIKSGIVTVIKDALLPSGT~~V~~

Fig. 29

MTRAPPSTVMAMGAATSPCKILSATQR~~A~~AAAPSASTSRESVCLLRAPRGRQRPRGLALSAPARRPV
 SPRAVSDSKSSQTCL~~D~~P~~A~~STSVLGI~~L~~GGGAGTR~~L~~YPLTKKRAKPAVPLGAN~~Y~~RLIDIPVSNC~~I~~NSNISK
 IYVL~~T~~QFNSASLNRHLSRAYGSNIGGYKNEG~~F~~V~~E~~LAQQSPDNPNWFQGTADA~~V~~RQYLWL~~F~~EEHN~~V~~MEY
 IL~~A~~GDHLYRMDYEKF~~I~~QAHRET~~D~~ADITVAALPMDEERATAFGLMKIDE~~E~~GRIVEFAEKPKGEQLKAMMVDT
 TT~~I~~LG~~L~~D~~D~~VRAKEM~~P~~YIAS~~M~~GIYV~~I~~SKHV~~M~~QLRDQ~~F~~PGANDFGSE~~V~~PGATSTGMRVQAYLYDGYWEDI
 TIEAFYNANLGITKKP~~I~~PDFSYDR~~S~~APIYTQPRHLPPSKVLDADVTDSV~~I~~GEGCVIKNC~~I~~HHSV~~V~~GLR
 C~~I~~SEGAI~~I~~EDTLLMGADYYETEADKLLADKG~~G~~PI~~I~~GIGKNSHIRRAI~~I~~DKNARIGDNV~~K~~IINV~~D~~NVQEA
 RETDGYFIKSGIVTVIKDALLPSGT~~V~~

Fig. 30

MAATMTVEEVRAKAQRAEGPATVLAIGTATPANC~~V~~YQADYPDYYFKITKSDHLADLKEKF~~K~~RMCDKSQIRKR
 YMHLTEEILEENPNMCAYMAPSLDARQDI~~V~~V~~V~~VP~~K~~LGKAA~~A~~QKAIKEWGQ~~P~~RSKITHLVFC~~T~~TS~~G~~V~~D~~MPG
 ADYQLT~~K~~MLGLRPSV~~K~~RLMMYQQGCFAGGT~~V~~L~~R~~IAKDLAENN~~R~~GA~~V~~LV~~V~~C~~S~~EITAVTFRGP~~H~~ES~~H~~LD~~S~~LV
 GQALFGD~~G~~AA~~A~~VI~~I~~GADPDVSVERPLFQLVS~~V~~SQ~~T~~ILPD~~S~~EGAIDG~~H~~REVGLTF~~H~~LLKD~~V~~PG~~L~~ISK~~N~~IER
 ALEEA~~F~~KPLGIDD~~W~~NSVFWAH~~P~~GGPA~~I~~LD~~M~~VEAKVNL~~N~~KERMRATR~~H~~VLSEYGNMSSAC~~V~~LFIMDEM~~R~~KR
 SAEDGHTT~~T~~GEGMDW~~G~~V~~L~~FGFGP~~G~~LT~~V~~ET~~V~~VLHS~~M~~PIA~~A~~DATA

Fig. 31

MATTMTVEEVRAKAQRAEGPATVLAIGTATPANC~~V~~YQADYPDYYFKITKSDHLADLKEKF~~K~~RMCDKSQIRKR
 YMHLTEEILEENPNMCAYMAPSLDARQDI~~V~~V~~V~~VP~~K~~LGKAA~~A~~QKAIKEWGQ~~P~~RSKITHLVFC~~T~~TS~~G~~V~~D~~MPG
 ADYQLT~~K~~MLGLRPSV~~K~~RLMMYQQGCFAGGT~~V~~L~~R~~IAKDLAENN~~R~~GA~~V~~LV~~V~~C~~S~~EITAVTFRGP~~H~~ES~~H~~LD~~S~~LV
 GQALFGD~~G~~AA~~A~~VI~~I~~GADPDVS~~V~~H~~P~~L~~F~~QLVS~~S~~Q~~T~~ILPD~~S~~EGAIDG~~H~~REVGLTF~~H~~LLKD~~V~~PG~~L~~ISK~~N~~IER
 ALEEA~~F~~KPLGIDD~~W~~NSVFWAH~~P~~GGPA~~I~~LD~~M~~VEAKVNL~~N~~KERMRATR~~H~~VLSEYGNMSSAC~~V~~LFIMDEM~~R~~KR
 SAEDGHTT~~T~~GEGMDW~~G~~V~~L~~FGFGP~~G~~LT~~V~~ET~~V~~VLHS~~M~~PIAAGATA

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Fig. 32

RADLEEEGSFDDAVAGCDYAFLVAAPVNLKAENPEKDMVEPAVG GTLNAMRSCVRAGTVKR VVLTSSVASV
 SARPLLQGDGHVLDEESWSDVDFLRAKATGHWGPVSKVLL EKAACAF AOA SGISLVTVC PVVVGKAPAV
 QVHTSVPDVLSPLSGDEAKIQILQHIERASGSISLVHVDDL C RAEVFLAEEEAVASGRYICCSLSTTAGVL
 ARFLSVKYPQYKVRTDRFGSPEKPRVC MSAKLV AEGFQYKYKTLDEIYDDVVEYGRALGILP

Fig. 33

MAAAGDGSRRKTACVTGGNGYIASALVKMLLEKG YAVKTTV RNPDDMEKN SHLKDLQALGP LEVFRADLQE
 EG SFDDAVAGCDYAFLVAAPVNLKAENPEKDMVEPAVG GTLNAMRSCVRAGTVKR VVLTSSVASV SARPLL
 QGDGHVLDEESWSDVDFLRAKATGHWGPVSKVLL EKAACAF AOA SGISLVTVC PVVVGKAPAVQVHTS
 PDVLSPLSGDEAKIQILQHIERASGSISLVHVDDL C RAEVFLAEEEAVASGRYICCSLSTTAGVLARFLSV
 KYPQYKVRTDRFGSPEKPRVC MSAKLV AEGFQYKYKTLDEIYDDVVEYGRALGILP

Fig. 34

FISVTVFYVVGLRQRDLVQAGVQGT LNMRSCVKAGTVKR VILTSSDSA VCQR PLEG DGHV LDEGSWS DVP
 YLRAE QPEAWGYAVSKVLMEEAAGKFAD ENGL GLV SVLPTFTLGAAPV SQARTS VPV VLSLLSGD EEQNL
 LEAMHLITESVSINHIDL C R A QVFLAENEASSGRYICSSHD TTVVQLARLLADKYPQYNVKSQRFDGSPE
 KPRVCLSSQKLIGEGFVYKYDDL GAI LDDL VEVYGR TTGILP

Fig. 35

MASAAGGRRKTACVTGGSGYIASALIKTLLDHGYAVKTTV RNPDDLEKTSHLKDLQAFGPLEI FRGELDVE
 GS FDDSVSGCDYVFLVAAPMDMGSINPERDLVQAGVQGT LNMRSCVKAGTVKR VILTSSDSA VCQR PLEG
 DGHV LDEGSWS DVPYLRAE QPEAWGYAVSKVLMEEAAGKFAD ENGL GLV SVLPTFTLGAAPV SQARTS VPV
 VLSLLSGD EEQNL LEAMHLITESVSINHIDL C R A QVFLAENEASSGRYICSSHD TTVVQLARLLADKYP
 QYNVKSQRFDGSPEKPRVCLSSQKLIGEGFVYKYDDL VEVYGR TTGILPFAAASI WFLFRGSSSG
 KKLSKLPLPPGP RGWPV LGNLPQVGAKPH TMAA LSSQFGPLFRLRGV AEVVVAASAKV ASQFL RAHDAN
 FSDRPNSGAEHVAYNQDLV FAPYGS RWR ALRKLCALHL FSAK ALD AL RAVRE AEVALMV KQ LKE SAPAG
 VVVGQEA NCAT NALARA AVGRRVFGGSAGEGARE F KDMV VELM QLAGV FNIGD FVP ALRW LD PQGV VARM
 KRLH RRYDAMMDGFISERDQRHNQAAADGERKD LLSV MLG YMRPDGGGEEEGISFNHTDIKALLLN LFTA
 GDTTSSTV EWA LELIRHKDVL TQA QRE LDDIV QDRLV TESD LPHLTFL TAVIKETF RLHP STPL SLP R
 VATEDCEVEGYRIPKGTT LLVNVWAIARDPASWGPDALEFRPARFLAGGLHESVDVKGSDYELIPFGAGR
I CAGL SWGLRMV TLMTATLV HAFDW SLVDGLTPEKLD MEEAYGLT QRAAPL MVRPI PRLL SSAYTV

Fig. 36

MDHRDV L VLLCSIAAASI WFLFRGSSSGKKLSK LPLPPGP RGWPV LGNLPQVGAKPH HTMAA LSQQFG
PLFRLRGV AEVVVAASAKV ASQFL RAHDAN FS DRPP NSGA EH VAYN YQDLV FAPYGS RWR ALRKLCALHL
FSAK ALD AL RAVRE AEVALMV KQ LKE SAPAG VVVGQEA NCAT NALARA AVGRRVFGGSAGEGARE F KDMV
VELM QLAGV FNIGD FVP ALRW LD PQGV VARM KRLH RRYDAMMDGFISERDQRHNQAAADGERKD LLSV MLG
YMRPDGGGEEEGISFNHTDIKALLLN LFTA GDTTSSTV EWA LELIRHKDVL TQA QRE LDDIV QDRLV
TESD LPHLTFL TAVIKETF RLHP STPL SLP R VATEDCEVEGYRIPKGTT LLVNVWAIARDPASWGPDALEF
RPARFLAGGLHESVDVKGSDYELIPFGAGR I CAGL SWGLRMV TLMTATLV HAFDW SLVDGLTPEKLD MEEAYGLT QRAAPL MVRPI PRLL SSAYTV

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Fig. 37

RSELAGMDIPLSLLLSTLAISATICYVFFRAGKGHRAPLPLPPGPRGPVGLGNLPQLGGKTHQTLHEMTKV
 YGPVLRRLRGSSVVVAGSAAVAEQFLRTHDAKFSSRPPNSGGEHMAYNYRDVVFAPYGPRWRAMRKVCAV
 NIFSARALDDLRLGREREAALMVRSLADAAKAGVAVAVGKAANVCTTNGLSRAAVGLRVFGSDGARDFKEI
 VLEVMEVGGVLNVGDFVPALRWLDPOGVVARLKKLHRRFDDMMNGIIAERRTGKTAVVVEEGKGDLGLLL
 AMVQEDKSLTGSEEDKITDTDVKALILNLFVAGTETTS*SIVEWAELIRHPDILKQAQEELDAVVGDR*
 VSES~~DLPRLTFN~~AIKIETFRLHPSTPLSLPRMASEECEVAGYHIPRGTELLNVVWGIARDPALWPDPLEY
 QPARFLPGGSHEVNDLKGGDFGLIPFGAGRICA~~GLSWGLRMVTITATLVHSFDWELPAGQTPDKLNME~~
 AFSLLLQR~~A~~VPLMVHPVPRLLPSAYEIS

Fig. 38

~~MR~~SELAGMDIPLP~~L~~LLLSTLAISATICYVFFRAGKGHRAPLPLPPGPRGPVGLGNLPQLGGKTHQTLHEMTK
 VYGPVLRLRRGSSVVVAGSAAVAEQFLRTHDAKFSSRPPNSGGEHMAYNYRDVVFAPYGPRWRAMRKVCA
 VNIFSARALDDLRLGREREAALMVRSLADAAKAGVAVAVGKAANVCTTNGLSRAAVGLRVFGSDGARDFKE
 I~~V~~LEVMEVGGVLNVGDFVPALRWLDPOGVVARLKKLHRRFDDMMNGIIAERRTGKTAVVVEEGKGDLGLLL
 LAMVQEDKSLTGSEEDKITDTDVKALILNLFVAGTETTS*SIVEWAELIRHPDILKQAQEELDAVVGDR*
 LVSES~~DLPRLTFN~~AIKIETFRLHPSTPLSLPRMASEECEVAGYHIPRGTELLNVVWGIARDPALWPDPLEY
 YQPARFLPGGSHEVNDLKGGDFGLIPFGAGRICA~~GLSWGLRMVTITATLVHSFDWELPAGQTPDKLNME~~
 EAFSLLLQR~~A~~VPLMVHPVPRLLPSAYEIS

Fig. 39

DIPLPL~~L~~LLLSTLAISATICYVFFRAGKTHQTLHEMTKVYGPVLRLRRGSSVVVAGSAAVAEQFLRTHDAKF
 SSRPPNSGGEHMAYNYQDIVFAPYGPRWRAMRKVCAVNIFSARALDDLRLGREREAALMVRSLADAAKAGA
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Fig. 40

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 C~~E~~EVAGYHIPRGTELLNVVWGIARDPSLWPDPLEYRPARFLPGGSHEVNDLKGGDFGLIPFGAGRICA
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Fig. 41

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Shenk, Michael Andrew
Glenn, Matthew
Norris, Michael Geoffrey
Saulsbury, Keith Martin
Hall, Claire
Forster, Richard L. S.

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<213> *Lolium perenne*

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<210> 8

<211> 973

<212> DNA

<213> Lolium perenne

<400> 8

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<210> 9

<211> 2019

<212> DNA

<213> Lolium perenne

<400> 9

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<210> 10

<211> 2457

<212> DNA

<213> Lolium perenne

<400> 10

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<210> 11

<211> 2143

<212> DNA

<213> *Lolium perenne*

<400> 11

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<210> 12

<211> 2033

<212> DNA

<213> *Lolium perenne*

<400> 12

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<210> 13

<211> 1866

<212> DNA

<213> *Lolium perenne*

<400> 13

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<210> 14

<211> 2058

<212> DNA

<213> *Lolium perenne*

<400> 14

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<210> 15

<211> 2167

<212> DNA

<213> *Lolium perenne*

<400> 15

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<210> 16

<211> 2179

<212> DNA

<213> Festuca arundinacea

<400> 16

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<210> 17
<211> 1961
<212> DNA
<213> *Lolium perenne*

<400> 17

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<210> 18
<211> 1959
<212> DNA
<213> *Lolium perenne*

<400> 18

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<210> 19

<211> 1954

<212> DNA

<213> Festuca arundinacea

<400> 19

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<213> Festuca arundinacea

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<213> Festuca arundinacea

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<211> 2042

<212> DNA

<213> Lolium perenne

<400> 25

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<211> 1930
<212> DNA
<213> Festuca arundinacea

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<210> 27
<211> 1911
<212> DNA
<213> Lolium perenne

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<210> 28

<211> 2039

<212> DNA

<213> *Lolium perenne*

<400> 28

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<210> 29

<211> 2063

<212> DNA

<213> *Festuca arundinacea*

<400> 29

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<211> 1815

<212> DNA

<213> Lolium perenne

<400> 30

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<210> 31

<211> 1873
<212> DNA
<213> *Festuca arundinacea*

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<210> 32
<211> 1494
<212> DNA
<213> *Festuca arundinacea*

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<210> 33
<211> 1661
<212> DNA
<213> Festuca arundinacea

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<210> 34
<211> 992
<212> DNA
<213> Festuca arundinacea

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<210> 35
<211> 1279
<212> DNA
<213> Festuca arundinacea

<400> 35		
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<210> 36

<211> 1206

<212> DNA

<213> *Lolium perenne*

<400> 36

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<210> 37

<211> 1463

<212> DNA

<213> *Lolium perenne*

<400> 37

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<210> 38

<211> 1606

<212> DNA

<213> Lolium perenne

<400> 38

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<210> 39

<211> 1708

<212> DNA

<213> Lolium perenne

<400> 39

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<210> 40
<211> 1747
<212> DNA

<213> Festuca arundinacea

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<210> 41
<211> 1763
<212> DNA
<213> Festuca arundinacea

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<210> 42
<211> 1673
<212> DNA
<213> Festuca arundinacea

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<212> DNA
<213> Festuca arundinacea

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<210> 44

<211> 1449

<212> DNA

<213> Lolium perenne

<400> 44

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<210> 45

<211> 473

<212> PRT

<213> Lolium perenne

<400> 45

Met Ala Ala Ala Ala Val Ala Pro Asp Ala Lys Ile Glu Lys Phe Arg

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20 25 30

Cys Ile Ser Leu Val Ser Arg Tyr Leu Ser Gly Glu Ala Glu Gln Ile

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Ile	420	Pro	Ser	Ile	Val	Glu	Leu	Asp	Ser	Leu	Lys	Val	Ser	Gly	Asp	Val
							420			425						430
Ser	435	Phe	Gly	Ser	Gly	Ile	Val	Leu	Lys	Gly	Asn	Val	Thr	Ile	Ala	Ala
							435			440						445
Lys	450	Ser	Gly	Val	Lys	Leu	Glu	Ile	Pro	Asp	Gly	Ala	Val	Leu	Glu	Asn
							450			455						460
Lys	465	Asp	Ile	Asn	Gly	Pro	Glu	Asp	Leu							
							465			470						

<210> 46

<211> 471

<212> PRT

<213> Festuca arundinacea

<400> 46

Met	1	Ala	Ala	Val	Ala	Ala	Asp	Ala	Lys	Ile	Glu	Lys	Phe	Arg	Asp	Ala
							5			10				15		
Val	20	Ala	Lys	Leu	Asp	Glu	Ile	Ser	Glu	Asn	Glu	Lys	Ala	Gly	Cys	Ile
							20			25				30		
Ser	35	Leu	Val	Ser	Arg	Tyr	Leu	Ser	Gly	Glu	Ala	Glu	Gln	Ile	Glu	Trp

Ser Lys Ile Gln Thr Pro Thr Asp Glu Val Val Val Pro Tyr Asp Thr
 50 55 60
 Leu Ala Pro Ala Pro Gln Asp Leu Asp Ala Met Lys Ala Leu Leu Asp
 65 70 75 80
 Lys Leu Val Val Leu Lys Leu Asn Gly Gly Leu Gly Thr Thr Met Gly
 85 90 95
 Cys Thr Gly Pro Lys Ser Val Ile Glu Val Arg Asn Gly Phe Thr Phe
 100 105 110
 Leu Asp Leu Ile Val Ile Gln Ile Glu Ser Leu Asn Lys Lys Tyr Gly
 115 120 125
 Cys Asp Val Pro Leu Leu Leu Met Asn Ser Phe Asn Thr His Asp Asp
 130 135 140
 Thr Gln Lys Ile Val Glu Lys Tyr Ser Asn Ser Asn Ile Asn Ile His
 145 150 155 160
 Thr Phe Asn Gln Ser Gln Tyr Pro Arg Ile Val Thr Glu Asp Phe Leu
 165 170 175
 Pro Leu Pro Ser Lys Gly Lys Ser Gly Lys Asp Gly Trp Tyr Pro Pro
 180 185 190
 Gly His Gly Asp Val Phe Pro Ser Leu Asn Asn Ser Gly Lys Leu Asp
 195 200 205
 Thr Leu Leu Ser Gln Gly Lys Glu Tyr Val Phe Val Ala Asn Ser Asp
 210 215 220
 Asn Leu Gly Ala Ile Val Asp Ile Lys Ile Leu Asn His Leu Ile Asn
 225 230 235 240
 Asn Gln Asn Glu Tyr Cys Met Glu Val Thr Pro Lys Thr Leu Ala Asp
 245 250 255
 Val Lys Gly Gly Thr Leu Ile Ser Tyr Glu Gly Arg Val Gln Leu Leu
 260 265 270
 Glu Ile Ala Gln Val Pro Asp Glu His Val Asn Glu Phe Lys Ser Ile
 275 280 285
 Glu Lys Phe Lys Ile Phe Asn Thr Asn Asn Leu Trp Val Asn Leu Lys
 290 295 300
 Ala Ile Lys Arg Leu Val Glu Ala Asp Ala Leu Lys Met Glu Ile Ile
 305 310 315 320
 Pro Asn Pro Lys Glu Val Asp Gly Val Lys Val Leu Gln Leu Glu Thr
 325 330 335
 Ala Ala Gly Ala Ala Ile Arg Phe Phe Glu Lys Ala Ile Gly Ile Asn
 340 345 350
 Gly Pro Arg Ser Arg Phe Leu Pro Val Lys Ala Thr Ser Asp Leu Leu
 355 360 365
 Leu Val Gln Ser Asp Leu Tyr Thr Leu Val Asp Gly Tyr Val Ile Arg
 370 375 380
 Asn Pro Ala Arg Val Lys Pro Ser Asn Pro Ser Ile Glu Leu Gly Pro
 385 390 395 400
 Glu Phe Lys Lys Val Ala Ser Phe Leu Ala Arg Phe Lys Ser Ile Pro
 405 410 415
 Ser Ile Val Glu Leu Asp Ser Leu Lys Val Ser Gly Asp Val Thr Phe
 420 425 430
 Gly Ser Gly Val Val Leu Lys Gly Asn Val Thr Ile Ala Ala Lys Ser
 435 440 445
 Gly Val Lys Leu Glu Ile Pro Asp Gly Ala Val Leu Glu Asn Lys Asp
 450 455 460
 Ile Asn Gly Pro Glu Asp Leu
 465 470

<210> 47
 <211> 535
 <212> PRT
 <213> Lolium perenne

<400> 47
 Cys Leu Arg Arg Arg Thr Tyr Ser Asn Ser Gly Asp Thr His Ala Asp
 1 5 10 15
 Pro Asn Gly Pro Val Tyr Tyr Gly Gly Trp Tyr His Leu Phe Tyr Gln
 20 25 30
 His Asn Pro Tyr Gly Asp Ser Trp Gly Asn Val Ser Trp Gly His Ala
 35 40 45
 Val Ser Lys Asp Leu Val Asn Trp Arg His Leu Pro Val Ala Leu Val

50		55		60											
Pro	Asp	Gln	Trp	Tyr	Asp	Ile	Asn	Gly	Val	Leu	Thr	Gly	Ser	Ile	Thr
65			70						75						80
Val	Leu	Pro	Asp	Gly	Arg	Val	Ile	Leu	Leu	Tyr	Thr	Gly	Asn	Thr	Asp
				85					90					95	
Thr	Phe	Ser	Gln	Val	Gln	Cys	Leu	Ala	Val	Pro	Ala	Asp	Pro	Ser	Asp
				100					105					110	
Pro	Leu	Leu	Arg	Ser	Trp	Ile	Lys	His	Pro	Ala	Asn	Pro	Ile	Leu	Phe
					115				120					125	
Pro	Pro	Pro	Gly	Ile	Gly	Leu	Lys	Asp	Phe	Arg	Asp	Pro	Leu	Thr	Ala
				130					135					140	
Trp	Phe	Glu	His	Ser	Asp	Asn	Thr	Trp	Arg	Thr	Ile	Ile	Gly	Ser	Lys
				145					150					155	160
Asp	Asp	Asp	Gly	His	Ala	Gly	Ile	Val	Leu	Ser	Tyr	Lys	Thr	Thr	Asp
					165				170					175	
Phe	Val	Asn	Tyr	Glu	Leu	Met	Pro	Gly	Asn	Met	His	Arg	Gly	Pro	Asp
				180					185					190	
Gly	Thr	Gly	Met	Tyr	Glu	Cys	Leu	Asp	Ile	Tyr	Pro	Val	Gly	Gly	Asn
				195					200					205	
Ser	Ser	Glu	Met	Leu	Gly	Gly	Asp	Ser	Ser	Pro	Glu	Val	Leu	Phe	Val
				210					215					220	
Leu	Lys	Glu	Ser	Ala	Asn	Asp	Glu	Trp	His	Asp	Tyr	Tyr	Ala	Leu	Gly
					225				230					235	240
Trp	Phe	Asp	Ala	Thr	Ala	Asn	Thr	Trp	Thr	Pro	Gln	Asp	Pro	Glu	Ala
					245				250					255	
Asp	Leu	Gly	Ile	Gly	Leu	Arg	Tyr	Asp	Trp	Gly	Lys	Tyr	Tyr	Ala	Ser
				260					265					270	
Lys	Ser	Phe	Tyr	Asp	Pro	Ile	Lys	Asn	Arg	Arg	Val	Val	Trp	Ala	Phe
				275					280					285	
Val	Gly	Glu	Thr	Asp	Ser	Glu	Gln	Ala	Asp	Lys	Ala	Lys	Gly	Trp	Ala
				290					295					300	
Ser	Leu	Met	Ser	Ile	Pro	Arg	Met	Val	Glu	Leu	Asp	Lys	Lys	Thr	Arg
					305				310					315	320
Thr	Asn	Leu	Ile	Gln	Trp	Pro	Val	Glu	Glu	Ile	Glu	Thr	Leu	Arg	Arg
					325				330					335	
Asn	Val	Thr	Asp	Leu	Gly	Gly	Ile	Thr	Val	Glu	Ala	Gly	Ser	Val	Ile
				340					345					350	
His	Leu	Pro	Leu	Gln	Gln	Gly	Gly	Gln	Leu	Asp	Ile	Glu	Ala	Ser	Phe
				355					360					365	
Arg	Leu	Asn	Ser	Ser	Asp	Ile	Asp	Ala	Leu	Asn	Glu	Ala	Asp	Val	Gly
					370				375					380	
Phe	Asn	Cys	Ser	Ser	Ser	Ala	Gly	Ala	Ala	Val	Arg	Gly	Ala	Leu	Gly
					385				390					395	400
Pro	Phe	Gly	Leu	Leu	Val	Phe	Ala	Asp	Gly	Arg	His	Glu	Gln	Thr	Ala
					405				410					415	
Ala	Tyr	Phe	Tyr	Val	Ser	Lys	Gly	Leu	Asp	Gly	Ser	Leu	Leu	Thr	His
				420					425					430	
Tyr	Cys	His	Asp	Glu	Ser	Arg	Ser	Thr	Arg	Ala	Lys	Asp	Val	Val	Ser
				435					440					445	
Arg	Val	Val	Gly	Gly	Gly	Thr	Val	Pro	Val	Leu	Asp	Gly	Glu	Thr	Phe
				450					455					460	
Val	Arg	Val	Leu	Val	Asp	His	Ser	Ile	Val	Gln	Ser	Phe	Val	Met	Gly
				465					470					475	480
Gly	Arg	Thr	Thr	Val	Thr	Ser	Arg	Ala	Tyr	Pro	Thr	Glu	Ala	Ile	Tyr
				485					490					495	
Ala	Ala	Ala	Gly	Val	Tyr	Leu	Phe	Asn	Asn	Ala	Thr	Ser	Ala	Thr	Ile
				500					505					510	
Thr	Ala	Glu	Gly	Leu	Val	Val	Tyr	Glu	Met	Ala	Ser	Ala	Glu	Ser	Gln
				515					520					525	
Ala	Phe	Leu	Ala	Asp	Asp	Met									
				530											

<210> 48

<211> 637

<212> PRT

<213> Lolium perenne

<400> 48

Met Glu Ser Ser Ala Val Val Val Pro Gly Thr Thr Ala Pro Leu Leu
 1 5 10 15
 Pro Tyr Asp Ser Arg Glu Asn Gln Ser Ser Gly Gly Gly Val Trp Trp
 20 25 30
 Arg Ala Cys Ala Ala Ser Ala Val Val Leu Leu Val Val Val Gly Phe
 35 40 45
 Phe Ala Gly Gly Arg Val Asp Leu Gly Gln Ala Gly Glu Val Ser Ala
 50 55 60
 Thr Ser Ser Val Pro Ala Ala Met Met Glu Ile Pro Arg Ser Arg Gly
 65 70 75 80
 Lys Asn Phe Gly Val Ser Glu Lys Ala Asp Gly Gly Phe Pro Trp Ser
 85 90 95
 Asn Ala Met Leu Gln Trp Gln His Thr Gly Phe His Phe Gln Pro Leu
 100 105 110
 Lys His Tyr Met Asn Asp Pro Asn Gly Pro Val Tyr Tyr Gly Gly Trp
 115 120 125
 Tyr His Leu Phe Tyr Gln His Asn Pro Tyr Gly Asp Ser Trp Gly Asn
 130 135 140
 Val Ser Trp Gly His Ala Val Ser Lys Asp Leu Val Asn Trp Arg His
 145 150 155 160
 Leu Pro Val Ala Leu Val Pro Asp Gln Trp Tyr Asp Ile Asn Gly Val
 165 170 175
 Leu Thr Gly Ser Ile Thr Val Leu Pro Asp Gly Arg Val Ile Leu Leu
 180 185 190
 Tyr Thr Gly Asn Thr Asp Thr Phe Ser Gln Val Gln Cys Leu Ala Val
 195 200 205
 Pro Ala Asp Pro Ser Asp Pro Leu Leu Arg Ser Trp Ile Lys His Pro
 210 215 220
 Ala Asn Pro Ile Leu Phe Pro Pro Pro Gly Ile Gly Leu Lys Asp Phe
 225 230 235 240
 Arg Asp Pro Leu Thr Ala Trp Phe Glu His Ser Asp Asn Thr Trp Arg
 245 250 255
 Thr Ile Ile Gly Ser Lys Asp Asp Asp Gly His Ala Gly Ile Val Leu
 260 265 270
 Ser Tyr Lys Thr Thr Asp Phe Val Asn Tyr Glu Leu Met Pro Gly Asn
 275 280 285
 Met His Arg Gly Pro Asp Gly Thr Gly Met Tyr Glu Cys Leu Asp Ile
 290 295 300
 Tyr Pro Val Gly Gly Asn Ser Ser Glu Met Leu Gly Gly Asp Ser Ser
 305 310 315 320
 Pro Glu Val Leu Phe Val Leu Lys Glu Ser Ala Asn Asp Glu Trp His
 325 330 335
 Asp Tyr Tyr Ala Leu Gly Trp Phe Asp Ala Thr Ala Asn Thr Trp Thr
 340 345 350
 Pro Gln Asp Pro Glu Ala Asp Leu Gly Ile Gly Leu Arg Tyr Asp Trp
 355 360 365
 Gly Lys Tyr Tyr Ala Ser Lys Ser Phe Tyr Asp Pro Ile Lys Asn Arg
 370 375 380
 Arg Val Val Trp Ala Phe Val Gly Glu Thr Asp Ser Glu Gln Ala Asp
 385 390 395 400
 Lys Ala Lys Gly Trp Ala Ser Leu Met Ser Ile Pro Arg Met Val Glu
 405 410 415
 Leu Asp Lys Lys Thr Arg Thr Asn Leu Ile Gln Trp Pro Val Glu Glu
 420 425 430
 Ile Glu Thr Leu Arg Arg Asn Val Thr Asp Leu Gly Gly Ile Thr Val
 435 440 445
 Glu Ala Gly Ser Val Ile His Leu Pro Leu Gln Gln Gly Gly Gln Leu
 450 455 460
 Asp Ile Glu Ala Ser Phe Arg Leu Asn Ser Ser Asp Ile Asp Ala Leu
 465 470 475 480
 Asn Glu Ala Asp Val Gly Phe Asn Cys Ser Ser Ser Ala Gly Ala Ala
 485 490 495
 Val Arg Gly Ala Leu Gly Pro Phe Gly Leu Leu Val Phe Ala Asp Gly
 500 505 510
 Arg His Glu Gln Thr Ala Ala Tyr Phe Tyr Val Ser Lys Gly Leu Asp
 515 520 525
 Gly Ser Leu Leu Thr His Tyr Cys His Asp Glu Ser Arg Ser Thr Arg
 530 535 540

Ala Lys Asp Val Val Ser Arg Val Val Gly Gly Thr Val Pro Val Leu
 545 550 555 560
 Asp Gly Glu Thr Phe Ser Val Arg Val Leu Val Asp His Ser Ile Val
 565 570 575
 Gln Ser Phe Val Met Gly Gly Arg Thr Thr Val Thr Ser Arg Ala Tyr
 580 585 590
 Pro Thr Glu Ala Ile Tyr Ala Ala Gly Val Tyr Leu Phe Asn Asn
 595 600 605
 Ala Thr Ser Ala Thr Ile Thr Ala Glu Gly Leu Val Val Tyr Glu Met
 610 615 620
 Ala Ser Ala Glu Ser Gln Ala Phe Leu Ala Asp Asp Met
 625 630 635

<210> 49

<211> 603

<212> PRT

<213> Lolium perenne

<400> 49
 Met Gly Ile Ala Glu Val Ala Leu His Thr Met Pro Gly Ala Phe Ala
 1 5 10 15
 Ser His Ser Pro Ala Ser Ser Leu Pro Leu Arg Thr Asp Thr Arg Ser
 20 25 30
 Leu Arg Lys Arg Gly Thr Asn Ser Phe Tyr Arg Thr Leu Gly Gly Pro
 35 40 45
 Pro Lys Phe Pro Glu Leu Arg Pro Val Glu Cys Gln Cys Gln Arg Ile
 50 55 60
 Asp Asp Leu Ala Gly Val Ile Glu Ala Gly Asn Gly Thr Trp Ala Thr
 65 70 75 80
 Asp Met Val Asn Lys Ala Ser Gln Val Leu Gly Asp Val Ala Val Pro
 85 90 95
 Gly Gln Ala Leu Gly Asn Ala Ser Leu Ser Gly Asp Pro Glu Lys
 100 105 110
 Val Leu Pro Arg Arg Arg Asn Leu Ser Ser Val Glu Asp Glu Ala Trp
 115 120 125
 Asp Leu Leu Arg Glu Ser Val Val Asn Tyr Cys Gly Ser Pro Val Gly
 130 135 140
 Thr Ile Ala Ala Asn Asp Pro Asn Asp Ser Asn Pro Ala Asn Tyr Asp
 145 150 155 160
 Gln Val Phe Ile Arg Asp Phe Ile Pro Ser Gly Ile Ala Phe Leu Leu
 165 170 175
 Lys Gly Glu Tyr Glu Ile Val Arg Asn Phe Ile Leu His Thr Leu Gln
 180 185 190
 Leu Gln Ser Trp Glu Lys Thr Met Asp Cys His Ser Pro Gly Gln Gly
 195 200 205
 Leu Met Pro Ala Ser Phe Lys Val Arg Thr Ile Pro Leu Asp Gly Asp
 210 215 220
 Glu Asn Ala Thr Glu Glu Val Leu Asp Pro Asp Phe Gly Glu Ala Ala
 225 230 235 240
 Ile Gly Arg Val Ala Pro Val Asp Ser Gly Leu Trp Trp Ile Ile Leu
 245 250 255
 Leu Arg Ala Tyr Gly Lys Cys Ser Gly Asp Leu Ser Val Gln Glu Arg
 260 265 270
 Ile Asp Val Gln Thr Gly Ile Lys Met Ile Leu Lys Leu Cys Leu Ala
 275 280 285
 Asp Gly Phe Asp Met Phe Pro Thr Leu Leu Val Thr Asp Gly Ser Cys
 290 295 300
 Met Ile Asp Arg Arg Met Gly Ile His Gly His Pro Leu Glu Ile Gln
 305 310 315 320
 Ala Leu Phe Tyr Ser Ala Leu Leu Ser Ala Arg Glu Met Leu Thr Pro
 325 330 335
 Glu Asp Gly Ser Ala Asp Leu Ile Arg Ala Leu Asn Asn Arg Leu Val
 340 345 350
 Ala Leu Ser Phe His Ile Arg Glu Tyr Tyr Trp Val Asp Met Gln Lys
 355 360 365
 Leu Asn Glu Ile Tyr Arg Tyr Lys Thr Glu Glu Tyr Ser Tyr Asp Ala
 370 375 380
 Val Asn Lys Phe Asn Ile Tyr Pro Asp Gln Val Ser Pro Trp Leu Val

385		390		395		400									
Glu	Trp	Ile	Pro	Pro	Lys	Gly	Gly	Tyr	Phe	Ile	Gly	Asn	Leu	Gln	Pro
					405				410					415	
Ala	His	Met	Asp	Phe	Arg	Phe	Phe	Ser	Leu	Gly	Asn	Leu	Trp	Ser	Ile
					420				425				430		
Val	Ser	Ser	Leu	Ala	Thr	Thr	Gln	Gln	Ser	His	Ala	Ile	Leu	Asp	Leu
					435				440			445			
Ile	Glu	Ser	Lys	Trp	Ser	Asp	Leu	Val	Ala	Glu	Met	Pro	Leu	Lys	Ile
					450				455			460			
Cys	Tyr	Pro	Ala	Leu	Glu	Asn	Leu	Glu	Trp	Lys	Ile	Ile	Thr	Gly	Ser
					465				470			475			480
Asp	Pro	Lys	Asn	Thr	Pro	Trp	Ser	Tyr	His	Asn	Gly	Gly	Ser	Trp	Pro
					485				490			495			
Thr	Leu	Leu	Trp	Gln	Leu	Thr	Val	Ala	Ser	Leu	Lys	Met	Asn	Arg	Pro
					500				505			510			
Glu	Ile	Ala	Ala	Lys	Ala	Val	Glu	Ile	Ala	Glu	Arg	Arg	Ile	Ala	Thr
					515				520			525			
Asp	Lys	Trp	Pro	Glu	Tyr	Tyr	Asp	Thr	Lys	Arg	Ala	Arg	Phe	Ile	Gly
					530				535			540			
Lys	Gln	Ser	Arg	Leu	Tyr	Gln	Thr	Trp	Ser	Ile	Ala	Gly	Tyr	Leu	Val
					545				550			555			560
Ala	Lys	Gln	Leu	Leu	Asp	Lys	Pro	Asp	Ala	Ala	Arg	Ile	Leu	Trp	Asn
					565				570			575			
Asp	Glu	Asp	Thr	Glu	Ile	Leu	Asn	Ala	Phe	Ser	Thr	Asn	Arg	Lys	Arg
					580				585			590			
Gly	Lys	Lys	Val	Leu	Lys	Lys	Thr	Tyr	Ile	Val					
					595				600						

<210> 50

<211> 556

<212> PRT

<213> Festuca arundinacea

<400>	50															
Asp	Pro	Phe	Arg	Ala	Ala	Leu	Ala	Pro	Ala	Ser	Pro	Pro	Leu	Glu	Ala	
1					5				10				15			
Pro	Pro	Leu	Asp	Glu	Leu	Pro	Thr	Ala	Pro	Ser	His	Ser	Glu	Pro	Ala	
					20				25				30			
Ser	Ala	Ala	Ala	Ala	Ala	Ala	Pro	Glu	Gln	Asp	Pro	Val	Asp	Leu	Gln	His
					35				40			45				
Glu	Glu	Leu	Asp	Gly	Leu	Lys	Ala	Gly	Val	Glu	Ala	Val	Arg	Ser	Arg	
					50				55			60				
Glu	Glu	Ser	Pro	Gln	Glu	Lys	Glu	Ala	Trp	Trp	Leu	Leu	Asn	Arg	Ala	
					65				70			75			80	
Val	Val	Asn	Tyr	Cys	Gly	Ser	Ala	Val	Gly	Thr	Val	Ala	Ala	Asn	Asp	
					85				90			95				
Pro	Ser	Thr	Ala	Asn	His	Met	Leu	Asn	Tyr	Asp	Gln	Val	Phe	Ile	Arg	
					100				105			110				
Asp	Phe	Val	Pro	Ser	Ala	Ile	Ala	Phe	Leu	Leu	Lys	Gly	Glu	Ser	Asp	
					115				120			125				
Ile	Val	Lys	Asn	Phe	Leu	Leu	His	Thr	Leu	Gln	Leu	Gln	Ser	Trp	Glu	
					130				135			140				
Lys	Thr	Val	Asp	Cys	Tyr	Ser	Pro	Gly	Gln	Gly	Leu	Met	Pro	Ala	Ser	
					145				150			155			160	
Phe	Lys	Val	Arg	Ser	Val	Pro	Leu	Asp	Gly	Asn	Asn	Glu	Ala	Phe	Glu	
					165				170			175				
Glu	Val	Leu	Asp	Pro	Asp	Phe	Gly	Glu	Ser	Ala	Ile	Gly	Arg	Val	Ala	
					180				185			190				
Pro	Val	Asp	Ser	Gly	Leu	Trp	Trp	Ile	Ile	Leu	Leu	Arg	Ala	Tyr	Gly	
					195				200			205				
Lys	Ile	Thr	Gly	Asp	Tyr	Ala	Leu	Gln	Glu	Arg	Val	Asp	Val	Gln	Thr	
					210				215			220				
Gly	Ile	Arg	Leu	Ile	Leu	Asn	Leu	Cys	Leu	Ser	Asp	Gly	Phe	Asp	Met	
					225				230			235			240	
Phe	Pro	Thr	Leu	Leu	Val	Thr	Asp	Gly	Ser	Cys	Met	Ile	Asp	Arg	Arg	
					245				250			255				
Met	Gly	Ile	His	Gly	His	Pro	Leu	Glu	Ile	Gln	Ala	Leu	Phe	Tyr	Ser	
					260				265			270				

Ala Leu Arg Cys Ala Arg Glu Met Val Asn Ile Asp Asp Gly Ser Lys
 275 280 285
 Asn Leu Ile Arg Val Ile Asn Asn Arg Leu Ser Ala Leu Ser Phe His
 290 295 300
 Ile Arg Glu Tyr Tyr Trp Val Asp Met Lys Lys Ile Asn Glu Ile Tyr
 305 310 315 320
 Arg Tyr Lys Thr Glu Glu Tyr Ser His Asp Ala Ile Asn Lys Phe Asn
 325 330 335
 Ile Tyr Pro Glu Gln Ile Pro Ser Trp Leu Ala Asp Trp Ile Pro Glu
 340 345 350
 Lys Gly Gly Tyr Leu Ile Gly Asn Leu Gln Pro Ala His Met Asp Phe
 355 360 365
 Arg Phe Phe Ser Leu Gly Asn Leu Trp Ala Ile Val Ser Ser Leu Ala
 370 375 380
 Thr Pro Lys Gln Ala Glu Gly Ile Leu Asn Leu Ile Glu Thr Lys Trp
 385 390 395 400
 Asp Asp Ile Val Ala Asn Met Pro Leu Lys Ile Cys Tyr Pro Ala Leu
 405 410 415
 Glu Tyr Glu Glu Trp Arg Ile Ile Thr Gly Cys Asp Pro Lys Asn Thr
 420 425 430
 Pro Trp Ser Tyr His Asn Gly Gly Ser Trp Pro Thr Leu Leu Trp Gln
 435 440 445
 Phe Thr Leu Ala Cys Ile Lys Met Gly Arg Pro Asp Leu Ala Arg Arg
 450 455 460
 Ala Val Glu Ala Val Glu Lys Arg Leu Ser Asp Asp Lys Trp Pro Glu
 465 470 475 480
 Tyr Tyr Asp Thr Arg Asn Gly Arg Phe Ile Gly Lys Gln Ser Arg Leu
 485 490 495
 Tyr Gln Thr Trp Thr Ile Ala Gly Phe Leu Ser Ser Lys Leu Leu Leu
 500 505 510
 Asp Cys Pro Glu Met Ala Ser Ile Leu Ile Cys Asp Glu Asp Leu Asp
 515 520 525
 Leu Leu Glu Gly Cys Ala Cys Gly Ala Asn Lys Ser Ala Arg Val Lys
 530 535 540
 Cys Ser Arg Arg Ala Ala Arg Ser Gln Val Leu Val
 545 550 555

<210> 51

<211> 621

<212> PRT

<213> Festuca arundinacea

<400> 51
 Met Ala Ala Ala Ala Ile Ser His Leu Arg Arg Gly Thr Gln Arg His
 1 5 10 15
 Ala Leu Leu Tyr Leu Ser Arg Arg His Phe Ser Asn Ser Pro Leu Thr
 20 25 30
 Ala Ala Ala Pro Leu Ala Ala Ala Ala Arg Arg Leu Leu Ser Thr Thr
 35 40 45
 Val Glu Ser Gly Thr Ser Ser Ala Ala Gly Ser Tyr Lys Pro Pro Pro
 50 55 60
 Leu Asp Pro Phe Arg Ala Ala Leu Ala Pro Ala Ser Pro Pro Leu Glu
 65 70 75 80
 Ser Pro Pro Leu Asp Glu Leu Pro Thr Ala Pro Ser His Ser Glu Pro
 85 90 95
 Ala Ser Ala Ala Ala Ala Pro Glu Gln Asp Pro Val Asp Leu Gln
 100 105 110
 His Glu Glu Leu Asp Gly Leu Lys Ala Gly Val Glu Ala Val Arg Ser
 115 120 125
 Arg Glu Glu Ser Pro Gln Glu Lys Glu Ala Trp Trp Leu Leu Asn Arg
 130 135 140
 Ala Val Val Asn Tyr Cys Gly Ser Ala Val Gly Thr Val Ala Ala Asn
 145 150 155 160
 Asp Pro Ser Thr Ala Asn His Met Leu Asn Tyr Asp Gln Val Phe Ile
 165 170 175
 Arg Asp Phe Val Pro Ser Ala Ile Ala Phe Leu Leu Lys Gly Glu Ser
 180 185 190
 Asp Ile Val Lys Asn Phe Leu Leu His Thr Leu Gln Leu Gln Ser Trp

Glu	Lys	Thr	Val	Asp	Cys	Tyr	Ser	Pro	Gly	Gln	Gly	Leu	Met	Pro	Ala
195						200									
210						215					220				
Ser	Phe	Lys	Val	Arg	Ser	Val	Pro	Leu	Asp	Gly	Asn	Asn	Glu	Ala	Phe
225						230					235				240
Glu	Glu	Val	Leu	Asp	Pro	Asp	Phe	Gly	Glu	Ser	Ala	Ile	Gly	Arg	Val
						245				250				255	
Ala	Pro	Val	Asp	Ser	Gly	Leu	Trp	Trp	Ile	Ile	Leu	Leu	Arg	Ala	Tyr
						260			265				270		
Gly	Lys	Ile	Thr	Gly	Asp	Tyr	Ala	Leu	Gln	Glu	Arg	Val	Asp	Val	Gln
						275			280				285		
Thr	Gly	Ile	Arg	Leu	Ile	Leu	Asn	Leu	Cys	Leu	Ser	Asp	Gly	Phe	Asp
						290			295				300		
Met	Phe	Pro	Thr	Leu	Leu	Val	Thr	Asp	Gly	Ser	Cys	Met	Ile	Asp	Arg
305						310					315				320
Arg	Met	Gly	Ile	His	His	Pro	Leu	Glu	Ile	Gln	Ala	Leu	Phe	Tyr	
						325				330				335	
Ser	Ala	Leu	Arg	Cys	Ala	Arg	Glu	Met	Val	Asn	Ile	Asp	Asp	Gly	Ser
						340			345				350		
Lys	Asn	Leu	Ile	Arg	Val	Ile	Asn	Asn	Arg	Leu	Ser	Ala	Leu	Ser	Phe
						355			360				365		
His	Ile	Arg	Glu	Tyr	Tyr	Trp	Val	Asp	Met	Lys	Lys	Ile	Asn	Glu	Ile
						370			375				380		
Tyr	Arg	Tyr	Lys	Thr	Glu	Glu	Tyr	Ser	His	Asp	Ala	Ile	Asn	Lys	Phe
385						390				395				400	
Asn	Ile	Tyr	Pro	Glu	Gln	Ile	Pro	Ser	Trp	Leu	Ala	Asp	Trp	Ile	Pro
						405				410				415	
Glu	Lys	Gly	Gly	Tyr	Leu	Ile	Gly	Asn	Leu	Gln	Pro	Ala	His	Met	Asp
						420			425				430		
Phe	Arg	Phe	Phe	Ser	Leu	Gly	Asn	Leu	Trp	Ala	Ile	Val	Ser	Ser	Leu
						435			440				445		
Ala	Thr	Pro	Lys	Gln	Ala	Glu	Gly	Ile	Leu	Asn	Leu	Ile	Glu	Thr	Lys
						450			455				460		
Trp	Asp	Asp	Ile	Val	Ala	Asn	Met	Pro	Leu	Lys	Ile	Cys	Tyr	Pro	Ala
465						470				475				480	
Leu	Glu	Tyr	Glu	Glu	Trp	Arg	Ile	Ile	Thr	Gly	Cys	Asp	Pro	Lys	Asn
						485			490				495		
Thr	Pro	Trp	Ser	Tyr	His	Asn	Gly	Gly	Ser	Trp	Pro	Thr	Leu	Leu	Trp
						500			505				510		
Gln	Phe	Thr	Leu	Ala	Cys	Ile	Lys	Met	Gly	Arg	Pro	Asp	Leu	Ala	Arg
						515			520				525		
Arg	Ala	Val	Glu	Ala	Val	Glu	Lys	Arg	Leu	Ser	Asp	Asp	Lys	Trp	Pro
						530			535				540		
Glu	Tyr	Tyr	Asp	Thr	Arg	Asn	Gly	Arg	Phe	Ile	Gly	Lys	Gln	Ser	Arg
						545			550				555		560
Leu	Tyr	Gln	Thr	Trp	Thr	Ile	Ala	Gly	Phe	Leu	Ser	Ser	Lys	Leu	Leu
						565			570				575		
Leu	Asp	Cys	Pro	Glu	Met	Ala	Ser	Ile	Leu	Ile	Cys	Asp	Glu	Asp	Leu
						580			585				590		
Asp	Leu	Leu	Glu	Gly	Cys	Ala	Cys	Gly	Ala	Asn	Lys	Ser	Ala	Arg	Val
						595			600				605		
Lys	Cys	Ser	Arg	Arg	Ala	Ala	Arg	Ser	Gln	Val	Leu	Val			
						610			615				620		

<210> 52

<211> 244

<212> PRT

<213> Lolium perenne

<400> 52

Leu	Leu	Glu	Lys	Arg	Lys	Leu	Asn	Glu	Ile	Tyr	Arg	Tyr	Lys	Thr	Glu
1				5					10				15		
Glu	Tyr	Ser	Tyr	Asp	Ala	Val	Asn	Lys	Phe	Asn	Ile	Tyr	Pro	Asp	Gln
						20			25				30		
Ile	Pro	Pro	Trp	Leu	Val	Glu	Trp	Ile	Pro	Pro	Lys	Gly	Gly	Tyr	Phe
						35			40				45		
Ile	Gly	Asn	Leu	Gln	Pro	Ala	His	Met	Asp	Phe	Arg	Phe	Phe	Ser	Leu
						50			55				60		

Gly Asn Leu Trp Ser Ile Val Ser Ser Leu Ala Thr Ala Asp Gln Ser
 65 70 75 80
 His Ala Ile Leu Asp Leu Val Glu Ala Lys Trp Ser Asp Leu Val Ala
 85 90 95
 Glu Met Pro Met Lys Ile Cys Tyr Pro Ala Leu Glu Asp Gln Glu Trp
 100 105 110
 Lys Phe Ile Thr Gly Ser Asp Pro Lys Asn Thr Pro Trp Ser Tyr His
 115 120 125
 Asn Gly Gly Ser Trp Pro Thr Leu Leu Trp Gln Leu Thr Val Ala Cys
 130 135 140
 Ile Lys Met Asn Arg Pro Glu Ile Ala Ala Arg Ala Val Glu Val Ala
 145 150 155 160
 Glu Ser Arg Ile Ser Met Asp Lys Trp Pro Glu Tyr Tyr Asp Thr Lys
 165 170 175
 Arg Gly Arg Phe Ile Gly Lys Gln Ala Arg Leu Phe Gln Thr Trp Ser
 180 185 190
 Ile Ala Gly Phe Leu Val Ala Lys Leu Leu Glu Asn Pro Glu Lys
 195 200 205
 Ser Arg Ile Leu Trp Asn Asn Glu Asp Glu Glu Ile Leu Asn Ala Leu
 210 215 220
 Ser Leu Met Thr Gly Pro Ser Ser Pro Lys Arg Lys Arg Gly Arg Lys
 225 230 235 240
 Thr Tyr Ile Val

<210> 53
 <211> 578
 <212> PRT
 <213> Lolium perenne

<400> 53
 Met Ala Ile Ala Ala Ala Ala Leu Leu Pro Leu His Leu Gly Cys
 1 5 10 15
 Ser Asp Ala Ala Pro Arg Arg Pro Gly Asn Ser Leu Arg Ala His Leu
 20 25 30
 Arg Lys Gly Gly Ile Arg Gly Arg Arg Ser Pro Pro Cys Ala Val
 35 40 45
 Asn Ser Leu His Pro Ser Gly Asn Pro Lys Thr Pro Gly Gly Asp
 50 55 60
 Val Gly Gly Ala Trp Gly Leu Asn Gly Ala Thr Ala Lys Pro Asp
 65 70 75 80
 His Ala Pro Pro Ser Gln Arg Arg Ala Pro Arg Asp Val Glu Glu
 85 90 95
 Glu Ala Trp Ala Leu Leu Arg Glu Ser Val Val Ser Tyr Cys Gly Ser
 100 105 110
 Pro Val Gly Thr Ile Ala Ala Cys Asp Pro Asn Asp Ala Ser Pro Leu
 115 120 125
 Asn Tyr Asp Gln Val Phe Ile Arg Asp Phe Val Pro Ser Gly Val Ala
 130 135 140
 Phe Leu Leu Lys Gly Glu His Glu Ile Val Arg Asn Phe Ile Leu His
 145 150 155 160
 Thr Leu Gln Leu Gln Ser Trp Glu Lys Thr Ile Asp Cys His Ser Pro
 165 170 175
 Gly Gln Gly Leu Met Pro Ala Ser Phe Lys Val Arg Val Val Pro Leu
 180 185 190
 Asp Gly Gly Asp Asp Gly Ala Thr Glu Glu Val Leu Asp Pro Asp Phe
 195 200 205
 Gly Glu Ala Ala Ile Gly Arg Val Ala Pro Val Asp Ser Gly Leu Trp
 210 215 220
 Trp Ile Ile Leu Leu Arg Ala Tyr Gly Lys Cys Ser Gly Asp Leu Ser
 225 230 235 240
 Phe His Glu Arg Val Asp Val Gln Thr Gly Ile Lys Leu Ile Leu Lys
 245 250 255
 Leu Cys Leu Ala Asp Gly Phe Asp Met Phe Pro Thr Leu Leu Val Thr
 260 265 270
 Asp Gly Ser Cys Met Met Asp Arg Arg Met Gly Ile His Gly His Pro
 275 280 285
 Leu Glu Ile Gln Ala Leu Phe Tyr Ser Ala Leu Leu Ser Ala Arg Glu

290	295	300
Met Leu Thr Pro Glu Asp Gly Ser Ala Asp Leu Ile Arg Ala Leu Asn	310	315
305		320
Ser Arg Leu Met Ala Leu Ser Phe His Ile Arg Glu Tyr Tyr Trp Leu	325	330
		335
Glu Lys Arg Lys Leu Asn Glu Ile Tyr Arg Tyr Lys Thr Glu Glu Tyr	340	345
		350
Ser Tyr Asp Ala Val Asn Lys Phe Asn Ile Tyr Pro Asp Gln Ile Pro	355	360
		365
Pro Trp Leu Val Glu Trp Ile Pro Pro Lys Gly Gly Tyr Phe Ile Gly	370	375
		380
Asn Leu Gln Pro Ala His Met Asp Phe Arg Phe Phe Ser Leu Gly Asn	385	390
		395
Leu Trp Ser Ile Val Ser Ser Leu Ala Thr Ala Asp Gln Ser His Ala	405	410
		415
Ile Leu Asp Leu Val Glu Ala Lys Trp Ser Asp Leu Val Ala Glu Met	420	425
		430
Pro Met Lys Ile Cys Tyr Pro Ala Leu Glu Asp Gln Glu Trp Lys Phe	435	440
		445
Ile Thr Gly Ser Asp Pro Lys Asn Thr Pro Trp Ser Tyr His Asn Gly	450	455
		460
Gly Ser Trp Pro Thr Leu Leu Trp Gln Leu Thr Val Ala Cys Ile Lys	465	470
		475
Met Asn Arg Pro Glu Ile Ala Ala Arg Ala Val Glu Val Ala Glu Ser	485	490
		495
Arg Ile Ser Met Asp Lys Trp Pro Glu Tyr Tyr Asp Thr Lys Arg Gly	500	505
		510
Arg Phe Ile Gly Lys Gln Ala Arg Leu Phe Gln Thr Trp Ser Ile Ala	515	520
		525
Gly Phe Leu Val Ala Lys Leu Leu Glu Asn Pro Glu Lys Ser Arg	530	535
		540
Ile Leu Trp Asn Asn Glu Asp Glu Glu Ile Leu Asn Ala Leu Ser Leu	545	550
		555
Met Thr Gly Pro Ser Ser Pro Lys Arg Lys Arg Gly Arg Lys Thr Tyr	565	570
		575
Ile Val		

<210> 54
<211> 619
<212> PRT
<213> Lolium perenne

<400> 54				
Met Asn Gly Gln Thr Thr Met Gly Leu Ala Ala Ala Ala Ala Ala	1	5	10	15
Val Arg Pro Cys Arg Arg Arg Leu Leu Ser Ser Ala Ser Ala Ala	20		25	30
Ala Ala Lys Ala Ser Ala Thr Pro Leu Phe Pro Arg Cys Ser His Pro	35		40	45
Gln His Gln His Ser Arg Arg Ile Pro Phe Leu Val Ser Ala Ala	50	55	60	
Ser His Thr Ser Gln Ser Asp Pro Ser Thr Thr Pro Thr Pro Val Thr	65	70	75	80
Ser Asp Pro Arg Ser Ala Val Ala Gly Asn Leu Pro Phe Phe Asp Arg	85		90	95
Val Leu Phe Pro Gly Ser Phe Pro Leu Glu Thr Pro Pro Val Glu Glu	100		105	110
Pro Ala Pro Ala Pro Pro Ala Asp Glu Ala Gln Ala Ser Ala Ser Pro	115		120	125
Val Arg Glu Glu Ser Asp Thr Glu Arg Glu Ala Trp Arg Leu Leu Arg	130		135	140
Arg Ala Val Val Ser Tyr Cys Gly Asp Pro Val Gly Thr Val Ala Ala	145		150	155
Glu Asp Pro Glu Cys Thr Glu Met Leu Asn Tyr Asp Gln Val Phe Ile	165		170	175
Arg Asp Phe Val Pro Ser Ala Leu Ala Phe Leu Met Arg Gly Glu Thr	180		185	190

Glu Ile Val Arg Asn Phe Leu Leu His Thr Leu Gln Leu Gln Ser Trp
 195 200 205
 Glu Lys Thr Val Asp Cys Tyr Ser Pro Gly Gln Gly Leu Met Pro Ala
 210 215 220
 Ser Phe Lys Ile Lys Thr Val Pro Leu Asp Glu Asn Asn Glu Ala Phe
 225 230 235 240
 Glu Glu Val Leu Asp Pro Asp Phe Gly Glu Ser Ala Ile Gly Arg Val
 245 250 255
 Ala Pro Val Asp Ser Gly Leu Trp Trp Ile Ile Leu Leu Arg Ala Tyr
 260 265 270
 Cys Lys Phe Thr Gly Asp Tyr Ser Leu Gln Glu Arg Val Asp Val Gln
 275 280 285
 Thr Gly Ile Lys Leu Ile Leu Ser Leu Cys Leu Thr Asp Gly Phe Asp
 290 295 300
 Met Phe Pro Thr Leu Leu Val Thr Asp Gly Ser Cys Met Ile Asp Arg
 305 310 315 320
 Arg Met Gly Ile His Gly His Pro Leu Glu Ile Gln Ala Leu Phe Tyr
 325 330 335
 Ser Ala Leu Arg Cys Ser Arg Glu Met Ile Val Met Asn Asp Gly Ser
 340 345 350
 Lys His Leu Leu Gln Ala Ile Asn Asn Arg Leu Ser Ala Leu Ser Phe
 355 360 365
 His Ile Arg Glu Tyr Tyr Trp Val Asp Met Lys Lys Ile Asn Glu Ile
 370 375 380
 Tyr Arg Tyr Lys Thr Glu Glu Tyr Ser His Asp Ala Thr Asn Lys Phe
 385 390 395 400
 Asn Ile Tyr Pro Glu Gln Ile Pro Ser Trp Leu Val Asp Trp Val Pro
 405 410 415
 Glu Lys Gly Tyr Leu Ile Gly Asn Leu Gln Pro Ala His Met Asp
 420 425 430
 Phe Arg Phe Phe Ser Leu Gly Asn Leu Trp Ala Ile Ser Ser Ser Leu
 435 440 445
 Thr Thr Pro Thr Gln Ala Glu Gly Ile Leu Ser Leu Ile Glu Glu Lys
 450 455 460
 Trp Asp Asp Leu Val Ala Asn Met Pro Leu Lys Ile Cys Tyr Pro Ala
 465 470 475 480
 Met Glu Asp Asp Glu Trp Arg Ile Val Thr Gly Ser Asp Pro Lys Asn
 485 490 495
 Thr Pro Trp Ser Tyr His Asn Gly Ser Trp Pro Thr Leu Leu Trp
 500 505 510
 Gln Phe Thr Leu Ala Cys Ile Lys Met Gly Arg Pro Glu Leu Ala Arg
 515 520 525
 Arg Ala Ile Ala Val Ala Glu Glu Lys Leu Ser Ala Asp Lys Trp Pro
 530 535 540
 Glu Tyr Tyr Asp Thr Arg Ser Gly Arg Phe Val Gly Lys Gln Ser Arg
 545 550 555 560
 Ser Tyr Gln Thr Trp Thr Ile Ala Gly Phe Leu Thr Ser Lys Ile Leu
 565 570 575
 Leu Glu Asn Pro Glu Leu Ala Ser Ile Leu Thr Cys Asp Glu Asp Leu
 580 585 590
 Glu Leu Leu Glu Gly Cys Ala Cys Cys Leu Ser Lys Arg Thr Arg Cys
 595 600 605
 Ser Arg Arg Val Thr Lys Ser Asp Ile Ile Gly
 610 615

<210> 55
 <211> 578
 <212> PRT
 <213> Lolium perenne

<400> 55
 Met Ala Ile Ala Ala Ala Ala Leu Leu Pro Leu His Leu Gly Cys
 1 5 10 15
 Ser Asp Ala Ala Pro Arg Arg Pro Gly Asn Ser Leu Arg Ala His Leu
 20 25 30
 Arg Lys Gly Gly Ile Arg Gly Arg Arg Arg Ser Pro Pro Cys Ala Val
 35 40 45
 Asn Ser Leu His Pro Ser Gly Asn Pro Lys Thr Pro Gly Gly Asp

50 55 60
 Val Gly Gly Arg Gly Val Asn Gly Gly Ala Thr Ala Lys Pro Asp
 65 70 75 80
 His Ala Pro Pro Ser Gln Arg Arg Arg Ala Pro Arg Asp Val Glu Glu
 85 90 95
 Glu Ala Trp Ala Leu Leu Arg Glu Ser Val Val Ser Tyr Cys Gly Ser
 100 105 110
 Pro Val Gly Thr Ile Ala Ala Cys Asp Pro Asn Asp Ala Ser Pro Leu
 115 120 125
 Asn Tyr Asp Gln Val Phe Ile Arg Asp Phe Val Pro Ser Gly Val Ala
 130 135 140
 Phe Leu Leu Lys Gly Glu His Glu Ile Val Arg Asn Phe Ile Leu His
 145 150 155 160
 Thr Leu Gln Leu Gln Ser Trp Glu Lys Thr Ile Asp Cys His Ser Pro
 165 170 175
 Gly Gln Gly Leu Met Pro Ala Ser Phe Lys Val Arg Val Val Pro Leu
 180 185 190
 Asp Gly Gly Asp Asp Gly Ala Thr Glu Glu Val Leu Asp Pro Asp Phe
 195 200 205
 Gly Glu Ala Ala Ile Gly Arg Val Ala Pro Val Asp Ser Gly Leu Trp
 210 215 220
 Trp Ile Ile Leu Leu Arg Ala Tyr Gly Lys Cys Ser Gly Asp Leu Ser
 225 230 235 240
 Phe His Glu Arg Val Asp Val Gln Thr Gly Ile Lys Leu Ile Leu Lys
 245 250 255
 Leu Cys Leu Ala Asp Gly Phe Asp Met Phe Pro Thr Leu Leu Val Thr
 260 265 270
 Asp Gly Ser Cys Met Met Asp Arg Arg Met Gly Ile His Gly His Pro
 275 280 285
 Leu Glu Ile Gln Ala Leu Phe Tyr Ser Ala Leu Leu Ser Ala Arg Glu
 290 295 300
 Met Leu Thr Pro Glu Asp Gly Ser Ala Asp Leu Ile Arg Ala Leu Asn
 305 310 315 320
 Ser Arg Leu Met Ala Leu Ser Phe His Ile Arg Glu Tyr Tyr Trp Leu
 325 330 335
 Glu Lys Arg Lys Leu Asn Glu Ile Tyr Arg Tyr Lys Thr Glu Glu Tyr
 340 345 350
 Ser Tyr Asp Ala Val Asn Lys Phe Asn Ile Tyr Pro Asp Gln Ile Pro
 355 360 365
 Pro Trp Leu Val Glu Trp Ile Pro Pro Lys Gly Gly Tyr Phe Ile Gly
 370 375 380
 Asn Leu Gln Pro Ala His Met Asp Phe Arg Phe Phe Ser Leu Gly Asn
 385 390 395 400
 Leu Trp Ser Ile Val Ser Ser Leu Ala Thr Ala Asp Gln Ser His Ala
 405 410 415
 Ile Leu Asp Leu Val Glu Ala Lys Trp Ser Asp Leu Val Ala Glu Met
 420 425 430
 Pro Met Lys Ile Cys Tyr Pro Ala Leu Glu Asp Gln Glu Trp Lys Phe
 435 440 445
 Ile Thr Gly Ser Asp Pro Lys Asn Thr Pro Trp Ser Tyr His Asn Gly
 450 455 460
 Gly Ser Trp Pro Thr Leu Leu Trp Gln Leu Thr Val Ala Cys Ile Lys
 465 470 475 480
 Met Asn Arg Pro Glu Ile Ala Ala Arg Ala Val Glu Val Ala Glu Ser
 485 490 495
 Arg Ile Ser Thr Asp Lys Trp Pro Glu Tyr Tyr Asp Thr Lys Arg Gly
 500 505 510
 Arg Phe Ile Gly Lys Gln Ala Arg Leu Phe Gln Thr Trp Ser Ile Ala
 515 520 525
 Gly Phe Leu Val Ala Lys Leu Leu Glu Asn Pro Glu Lys Ser Arg
 530 535 540
 Ile Leu Trp Asn Asn Glu Asp Glu Glu Ile Leu Asn Ala Leu Ser Leu
 545 550 555 560
 Met Thr Gly Pro Ser Ser Pro Lys Arg Lys Arg Gly Arg Lys Thr Tyr
 565 570 575
 Ile Val

<210> 56
<211> 554
<212> PRT
<213> *Lolium perenne*

<400> 56
Met Lys Arg Val Ser Ser His Val Ser Ile Ala Ser Glu Ala Glu Ile
1 5 10 15
Asn Leu Asp Leu Ser Arg Leu Leu Ile Asp Lys Pro Arg Tyr Thr Leu
20 25 30
Glu Arg Lys Arg Ser Phe Asp Glu Gln Ser Trp Ser Glu Leu Thr His
35 40 45
Thr His Arg Gln Asn Asp Gly Phe Asp Ser Val Leu Gln Ser Pro Ala
50 55 60
Phe Arg Thr Gly Phe Asp Ser Pro Phe Ser Met Gly Thr His Phe Gly
65 70 75 80
Glu Pro Ser Gly Pro His Pro Leu Val Asn Glu Ala Trp Glu Ala Leu
85 90 95
Arg Lys Ser Val Val Tyr Phe Arg Gly Gln Pro Val Gly Thr Ile Ala
100 105 110
Ala Val Asp His Ala Ser Glu Glu Val Leu Asn Tyr Asp Gln Val Phe
115 120 125
Val Arg Asp Phe Val Pro Ser Ala Leu Ala Phe Leu Met Asn Asn Glu
130 135 140
Pro Glu Ile Val Lys Asn Phe Leu Leu Lys Thr Leu His Leu Gln Ser
145 150 155 160
Ser Glu Lys Met Val Asp Arg Phe Lys Leu Gly Ala Gly Ala Met Pro
165 170 175
Ala Ser Phe Lys Val Asp Arg Asn Lys Ser Arg Asn Thr Glu Thr Leu
180 185 190
Val Ala Asp Phe Gly Glu Ser Ala Ile Gly Arg Val Ala Pro Val Asp
195 200 205
Ser Gly Phe Trp Trp Ile Ile Leu Leu Arg Ala Tyr Thr Lys Tyr Thr
210 215 220
Gly Asp Ala Ser Leu Ser Glu Ser Pro Asp Cys Gln Lys Cys Met Arg
225 230 235 240
Leu Ile Leu Asn Leu Cys Leu Ser Glu Gly Phe Asp Thr Phe Pro Thr
245 250 255
Leu Leu Cys Thr Asp Gly Cys Ser Met Ile Asp Arg Arg Met Gly Ile
260 265 270
Tyr Gly Tyr Pro Ile Glu Ile Gln Ala Leu Phe Tyr Met Ala Leu Arg
275 280 285
Cys Ala Leu Gln Met Leu Lys Pro Asp Gly Glu Gly Lys Asp Phe Ile
290 295 300
Glu Lys Ile Gly Gln Arg Leu His Ala Leu Thr Tyr His Met Arg Asn
305 310 315 320
Tyr Phe Trp Leu Asp Phe Pro His Leu Asn Asn Ile Tyr Arg Tyr Lys
325 330 335
Thr Glu Glu Tyr Ser His Thr Ala Val Asn Lys Phe Asn Val Ile Pro
340 345 350
Asp Ser Ile Pro Asp Trp Val Phe Asp Phe Met Pro Cys Arg Gly Gly
355 360 365
Tyr Phe Leu Gly Asn Val Ser Pro Ala Met Met Asp Phe Arg Trp Phe
370 375 380
Ala Leu Gly Asn Cys Ile Ala Ile Ile Ser Ser Leu Ala Thr Pro Glu
385 390 395 400
Gln Ser Ser Ala Ile Met Asp Leu Ile Glu Glu Arg Trp Asp Glu Leu
405 410 415
Val Gly Glu Val Pro Leu Lys Ile Cys Tyr Pro Ala Ile Glu Asn His
420 425 430
Glu Trp Arg Ile Ile Thr Gly Cys Asp Pro Lys Asn Thr Arg Trp Ser
435 440 445
Tyr His Asn Gly Gly Ser Trp Pro Val Leu Leu Trp Leu Leu Thr Ala
450 455 460
Ala Cys Ile Lys Thr Gly Arg Pro Gln Met Ala Lys Arg Ala Ile Glu
465 470 475 480
Leu Ser Glu Ala Arg Leu Leu Lys Asp Gly Trp Pro Glu Tyr Tyr Asp
485 490 495

Gly Lys Leu Gly Lys Phe Val Gly Lys Gln Ala Arg Lys Phe Gln Thr
 500 505 510
 Trp Ser Ile Ala Gly Tyr Leu Val Ala Arg Met Met Leu Glu Asp Pro
 515 520 525
 Ser Thr Leu Met Met Ile Ser Met Glu Glu Asp Arg Pro Val Lys Pro
 530 535 540
 Thr Met Arg Arg Ser Ala Ser Trp Asn Ala
 545 550

<210> 57
 <211> 552
 <212> PRT
 <213> Lolium perenne

<400> 57
 Met Glu Ala Pro Gly Gly Ala Gly Pro Met Pro Thr Thr Pro Ser
 1 5 10 15
 His Ala Ser Ile Ala Asp Ser Asp Asp Phe Asp Leu Ser Arg Leu Leu
 20 25 30
 Asn His Arg Pro Arg Ile Asn Val Glu Arg Gln Arg Ser Phe Asp Asp
 35 40 45
 Arg Ser Leu Gly Asp Leu Tyr Leu Ser Ala Met Asp Ser Arg Gly Gly
 50 55 60
 Tyr Met Asp Ser Tyr Asp Ser Met Tyr Ser Pro Gly Gly Leu Arg
 65 70 75 80
 Ser Leu Thr Gly Thr Pro Ala Ser Ser Thr Arg Leu Ser Phe Glu Pro
 85 90 95
 Gln Leu Leu Val Ala Glu Ala Trp Glu Ala Leu Arg Arg Ser Leu Val
 100 105 110
 Cys Phe Arg Gly Glu Pro Leu Gly Thr Ile Ala Ala Val Asp Ser Ser
 115 120 125
 Ser Asp Glu Val Leu Asn Tyr Asp Gln Val Phe Val Arg Asp Phe Val
 130 135 140
 Pro Ser Ala Leu Ala Phe Leu Met Asn Gly Glu Pro Asp Ile Val Lys
 145 150 155 160
 Asn Phe Leu Leu Lys Thr Leu Leu Leu Gln Gly Trp Glu Lys Arg Ile
 165 170 175
 Asp Arg Phe Lys Leu Gly Glu Gly Ala Met Pro Ala Ser Phe Lys Val
 180 185 190
 Leu Lys Asp Pro Lys Arg Gly Val Asp Thr Leu Ala Ala Asp Phe Gly
 195 200 205
 Glu Ser Ala Ile Gly Arg Val Ala Pro Ala Asp Ser Gly Phe Trp Trp
 210 215 220
 Ile Ile Leu Leu Arg Ala Tyr Thr Lys Ser Thr Gly Asp Leu Thr Leu
 225 230 235 240
 Ala Glu Thr Pro Glu Cys Gln Lys Gly Ile Arg Leu Ile Met Asn Gln
 245 250 255
 Cys Leu Ala Glu Gly Phe Asp Thr Phe Pro Thr Leu Leu Cys Ala Asp
 260 265 270
 Gly Cys Cys Met Ile Asp Arg Arg Met Gly Val Tyr Gly Tyr Pro Ile
 275 280 285
 Glu Ile Gln Ala Leu Phe Phe Met Ser Leu Arg Cys Ala Leu Leu Leu
 290 295 300
 Leu Lys Pro Ala Val Glu Gly Asn Ser Ser Ser Lys Asp Asp Asp Ile
 305 310 315 320
 Met Glu Arg Ile Val Thr Arg Leu His Ala Leu Ser Tyr His Met Arg
 325 330 335
 Ser Tyr Phe Trp Leu Asp Phe Gln Gln Leu Asn Val Ile Tyr Arg Phe
 340 345 350
 Lys Thr Glu Glu Tyr Ser His Thr Ala Val Asn Lys Phe Asn Val Ile
 355 360 365
 Pro Glu Ser Ile Pro Asp Trp Leu Phe Asp Phe Met Pro Ser Arg Gly
 370 375 380
 Gly Tyr Phe Val Gly Asn Val Ser Pro Ala Arg Met Asp Phe Arg Trp
 385 390 395 400
 Phe Ala Leu Gly Asn Cys Val Ala Ile Leu Ala Ser Leu Ala Thr Pro
 405 410 415
 Glu Gln Ala Gly Ala Ile Met Asp Leu Ile Glu Glu Arg Trp Glu Asp

Leu Ile Gly Glu Met Pro Leu Lys Ile Cys Tyr Pro Thr Ile Glu Gly
 420 425 435 440 445 450 455 460 465 470 475 480 485 490 495
 His Glu Trp Gln Asn Val Thr Gly Cys Asp Pro Lys Asn Thr Arg Trp
 495 500 505 510 515 520 525
 Ser Tyr His Asn Gly Gly Ser Trp Pro Val Leu Ile Trp Leu Leu Thr
 Ala Ala Cys Ile Lys Thr Gly Arg Leu Lys Ile Ala Arg Arg Ala Ile
 Asp Leu Ala Glu Ala Arg Leu Gly Lys Asp Gly Trp Pro Glu Tyr Tyr
 500 505 510
 Asp Gly Lys Leu Gly Arg Tyr Val Gly Lys Gln Ala Arg Lys His Gln
 515 520 525
 Thr Trp Ser Ile Ala Gly Tyr Leu Val Ala Lys Met Met Leu Glu Asp
 530 535 540
 Pro Ser His Leu Gly Met Ile Ser
 545 550

<210> 58
 <211> 562
 <212> PRT
 <213> Lolium perenne

<400> 58
 Met Glu Phe Gly Ala Pro Gly Gly Met Arg Arg Ser Ala Ser His Asn
 1 5 10 15
 Ser Leu Ser Gly Ser Asp Asp Phe Asp Leu Thr His Leu Leu Asn Lys
 20 25 30
 Pro Arg Ile Asn Val Glu Arg Gln Arg Ser Phe Asp Asp Arg Ser Leu
 35 40 45
 Ser Asp Val Ser Tyr Ser Gly Gly His Ala Arg Gly Ala Gly Gly
 50 55 60
 Gly Phe Asp Gly Met Tyr Ser Pro Gly Gly Leu Arg Ser Leu Val
 65 70 75 80
 Gly Thr Pro Ala Ser Ser Ala Leu His Ser Phe Glu Pro His Pro Ile
 85 90 95
 Val Gly Asp Ala Trp Glu Ala Leu Arg Arg Ser Leu Val Phe Phe Arg
 100 105 110
 Gly Gln Pro Leu Gly Thr Ile Ala Ala Tyr Asp His Ala Ser Glu Glu
 115 120 125
 Val Leu Asn Tyr Asp Gln Val Phe Val Arg Asp Phe Val Pro Ser Ala
 130 135 140
 Met Ala Phe Leu Met Asn Gly Glu Pro Glu Ile Val Lys Asn Phe Leu
 145 150 155 160
 Leu Lys Thr Val Leu Leu Gln Gly Trp Glu Lys Lys Val Asp Arg Phe
 165 170 175
 Lys Leu Gly Glu Gly Ala Met Pro Ala Ser Phe Lys Val Leu His Asp
 180 185 190
 Asp Lys Lys Gly Val Asp Thr Leu His Ala Asp Phe Gly Glu Ser Ala
 195 200 205
 Ile Gly Arg Val Ala Pro Val Asp Ser Gly Phe Trp Trp Ile Ile Leu
 210 215 220
 Leu Arg Ala Tyr Thr Lys Ser Thr Gly Asp Leu Thr Leu Ala Glu Lys
 225 230 235 240
 Pro Glu Cys Gln Lys Ala Met Arg Leu Ile Leu Ser Leu Cys Leu Ser
 245 250 255
 Glu Gly Phe Asp Thr Phe Pro Thr Leu Leu Cys Ala Asp Gly Cys Cys
 260 265 270
 Met Ile Asp Arg Arg Met Gly Val Tyr Gly Tyr Pro Ile Glu Ile Gln
 275 280 285
 Ser Leu Phe Phe Met Ala Leu Arg Cys Ala Leu Leu Met Leu Lys His
 290 295 300
 Asp Asn Glu Gly Lys Asp Phe Val Glu Arg Ile Ala Thr Arg Leu His
 305 310 315 320
 Ala Leu Ser Tyr His Met Arg Ser Tyr Phe Trp Leu Asp Phe Gln Gln
 325 330 335
 Leu Asn Asp Ile Tyr Arg Tyr Lys Thr Glu Glu Tyr Ser His Thr Ala
 340 345 350

Val Asn Lys Phe Asn Val Ile Pro Asp Ser Ile Pro Asp Trp Leu Phe
 355 360 365
 Asp Phe Met Pro Cys Glu Gly Phe Phe Val Gly Asn Val Ser Pro
 370 375 380
 Ala Arg Met Asp Phe Arg Trp Phe Ala Leu Gly Asn Met Ile Ala Ile
 385 390 395 400
 Val Ser Ser Leu Ala Thr Pro Glu Gln Ser Thr Ala Ile Met Asp Leu
 405 410 415
 Ile Glu Glu Arg Trp Glu Glu Leu Ile Gly Glu Met Pro Leu Lys Ile
 420 425 430
 Cys Tyr Pro Ala Ile Glu Asn His Glu Trp Arg Ile Val Thr Gly Cys
 435 440 445
 Asp Pro Lys Asn Thr Arg Trp Ser Tyr His Asn Gly Gly Ser Trp Pro
 450 455 460
 Val Leu Leu Trp Leu Leu Thr Ala Ala Ser Ile Lys Thr Gly Arg Pro
 465 470 475 480
 Gln Ile Ala Arg Arg Ala Ile Asp Leu Ala Glu Arg Arg Leu Leu Lys
 485 490 495
 Asp Gly Trp Pro Glu Tyr Tyr Asp Gly Lys Leu Gly Lys Tyr Val Gly
 500 505 510
 Lys Gln Ala Arg Lys Phe Gln Thr Trp Ser Ile Ala Gly Tyr Leu Val
 515 520 525
 Ala Lys Met Leu Leu Glu Asp Pro Ser His Leu Gly Met Ile Ala Leu
 530 535 540
 Glu Glu Asp Lys Ala Met Lys Pro Val Leu Arg Arg Ser Ala Ser Trp
 545 550 555 560
 Thr Asn

<210> 59
 <211> 616
 <212> PRT
 <213> Lolium perenne

<400> 59
 Met Asp Ser Asp Tyr Gly Val Pro Arg Glu Leu Ser Glu Val Gln Lys
 1 5 10 15
 Lys Arg Thr Leu Tyr Gln Pro Asp Leu Pro Pro Cys Leu Gln Gly Thr
 20 25 30
 Thr Val Arg Val Glu Tyr Gly Asp Val Ala Ile Ala Ala Asp Pro Ala
 35 40 45
 Gly Ala His Val Ile Ser His Ala Phe Pro His Thr Tyr Gly Gln Pro
 50 55 60
 Leu Ala His Phe Leu Arg Lys Ala Ala Asn Val Ala Asp Ala Lys Val
 65 70 75 80
 Ile Ser Glu His Pro Ala Val Arg Val Gly Ile Val Phe Cys Gly Arg
 85 90 95
 Gln Ser Pro Gly Gly His Asn Val Ile Trp Gly Leu His Asp Ala Ile
 100 105 110
 Lys Ala His Asn Pro Asn Ser Lys Leu Ile Gly Phe Leu Gly Gly Ser
 115 120 125
 Asp Gly Leu Leu Ala Gln Lys Thr Leu Glu Ile Thr Asp Glu Val Leu
 130 135 140
 Ser Ser Tyr Lys Asn Gln Gly Tyr Asp Met Leu Gly Arg Thr Lys
 145 150 155 160
 Asp Gln Ile Arg Thr Thr Glu Gln Val Asn Gly Ala Met Ala Ser Cys
 165 170 175
 Gln Ala Leu Lys Leu Asp Ala Leu Ile Ile Gly Gly Val Thr Ser
 180 185 190
 Asn Thr Asp Ala Ala Gln Leu Ala Glu Thr Phe Ala Glu Ala Lys Cys
 195 200 205
 Ala Thr Lys Val Val Gly Val Pro Val Thr Leu Asn Gly Asp Leu Lys
 210 215 220
 Asn Gln Phe Val Glu Thr Val Gly Phe Asp Thr Ile Cys Lys Val
 225 230 235 240
 Asn Ser Gln Leu Ile Ser Asn Met Cys Thr Asp Ala Leu Ser Ala Glu
 245 250 255
 Lys Tyr Tyr Tyr Phe Ile Arg Met Met Gly Arg Lys Ala Ser His Val

Ala Leu Glu Cys Ala Leu Gln Ser His Pro Asn Met Val Ile Leu Gly
 260 265 270
 275 280 285
 Glu Glu Val Ala Ala Ser Lys Leu Thr Ile Phe Asp Ile Thr Lys Gln
 290 295 300
 Ile Cys Asp Ala Val Gln Ala Arg Ala Glu Lys Asp Lys Asn His Gly
 305 310 315 320
 Val Ile Leu Ile Pro Glu Gly Leu Val Glu Ser Ile Pro Glu Leu Tyr
 325 330 335
 Ala Leu Leu Gln Glu Ile Asn Gly Leu His Gly Lys Val Ser Ile
 340 345 350
 Glu Asn Ile Ser Ser Gln Leu Ser Pro Trp Ala Ser Ala Leu Phe Glu
 355 360 365
 Phe Leu Pro Gln Phe Ile Arg Gln Gln Leu Leu Leu Arg Pro Glu Ser
 370 375 380
 Asp Asp Ser Ala Gln Leu Ser Gln Ile Glu Thr Glu Lys Leu Leu Ala
 385 390 395 400
 Gln Leu Val Glu Thr Glu Met Asn Lys Arg Leu Lys Glu Gly Thr Tyr
 405 410 415
 Lys Gly Lys Phe Asn Ala Ile Cys His Phe Phe Gly Tyr Gln Ala
 420 425 430
 Arg Gly Ala Met Pro Ser Lys Phe Asp Cys Asp Tyr Ala Tyr Val Leu
 435 440 445
 Gly His Val Ser Tyr His Ile Leu Ala Ala Gly Leu Asn Gly Tyr Met
 450 455 460
 Ala Thr Val Thr Asn Leu Lys Ser Pro Leu Asn Lys Trp Arg Cys Gly
 465 470 475 480
 Ala Ala Pro Ile Ser Ser Met Met Thr Val Lys Arg Trp Ser Arg Gly
 485 490 495
 Pro Ser Thr Thr Gln Ile Gly Lys Pro Ala Val His Met Ala Ser Val
 500 505 510
 Asp Leu Arg Gly Lys Ala Tyr Glu Leu Leu Arg Gln Asn Ser Ser Ser
 515 520 525
 Cys Leu Leu Glu Asp Ile Tyr Arg Asn Pro Gly Pro Leu Gln Phe Glu
 530 535 540
 Gly Pro Gly Ser Asp Ser Lys Pro Ile Ser Leu Cys Val Glu Asp Gln
 545 550 555 560
 Asp Tyr Met Gly Arg Ile Lys Lys Leu Gln Glu Tyr Leu Glu Lys Val
 565 570 575
 Lys Ser Ile Val Lys Pro Gly Cys Ser Gln Asp Val Leu Lys Ala Ala
 580 585 590
 Leu Ser Ala Met Ser Ser Val Thr Asp Thr Leu Ala Ile Met Thr Ser
 595 600 605
 Ser Ser Thr Gly Gln Ala Pro Leu
 610 615

<210> 60

<211> 616

<212> PRT

<213> Festuca arundinacea

<400> 60

Met Asp Ser Asp Tyr Gly Val Pro Arg Glu Leu Ser Glu Val Gln Lys
 1 5 10 15
 Lys Arg Thr Leu Tyr Gln Pro Glu Leu Pro Pro Cys Leu Gln Gly Thr
 20 25 30
 Thr Val Arg Val Glu Tyr Gly Asp Val Ala Ile Ala Ala Asp Pro Ala
 35 40 45
 Gly Ala His Val Ile Ser His Ala Phe Pro His Thr Tyr Gly Gln Pro
 50 55 60
 Leu Ala His Phe Leu Arg Lys Ala Ala Asn Val Ala Asp Ala Lys Val
 65 70 75 80
 Ile Ser Glu His Pro Ala Val Arg Val Gly Ile Val Phe Cys Gly Arg
 85 90 95
 Gln Ser Pro Gly Gly His Asn Val Ile Trp Gly Leu His Asp Ala Ile
 100 105 110
 Lys Ala His Asn Ser Asn Ser Lys Leu Ile Gly Phe Leu Gly Gly Ser
 115 120 125

Asp Gly Leu Leu Ala Gln Lys Thr Leu Glu Ile Thr Asp Glu Val Leu
 130 135 140
 Ser Ser Tyr Lys Asn Gln Gly Gly Tyr Asp Met Leu Gly Arg Thr Lys
 145 150 155 160
 Asp Gln Ile Arg Thr Thr Glu Gln Val Asn Gly Ala Met Ala Ser Cys
 165 170 175
 Gln Asp Leu Lys Leu Asp Ala Leu Ile Ile Gly Gly Val Thr Ser
 180 185 190
 Asn Thr Asp Ala Ala Gln Leu Ala Glu Thr Phe Ala Glu Ala Lys Cys
 195 200 205
 Ala Thr Lys Val Val Gly Val Pro Val Thr Leu Asn Gly Asp Leu Lys
 210 215 220
 Asn Gln Phe Val Glu Thr Thr Val Gly Phe Asp Thr Ile Cys Lys Val
 225 230 235 240
 Asn Ser Gln Leu Ile Ser Asn Met Cys Thr Asp Ala Leu Ser Ala Glu
 245 250 255
 Lys Tyr Tyr Phe Ile Arg Met Met Gly Arg Lys Ala Ser His Val
 260 265 270
 Ala Leu Glu Cys Ala Leu Gln Ser His Pro Asn Met Val Ile Leu Gly
 275 280 285
 Glu Glu Val Ala Ala Ser Lys Leu Thr Ile Phe Asp Ile Thr Lys Gln
 290 295 300
 Ile Cys Asp Ala Val Gln Ala Arg Ala Glu Lys Asp Lys Asn His Gly
 305 310 315 320
 Val Ile Leu Ile Pro Glu Gly Leu Val Glu Ser Ile Pro Glu Leu Tyr
 325 330 335
 Ala Leu Leu Gln Glu Ile Asn Gly Leu His Gly Lys Gly Val Ser Ile
 340 345 350
 Glu Asn Ile Ser Ser Gln Leu Ser Pro Trp Ala Ser Ala Leu Phe Glu
 355 360 365
 Phe Leu Pro Gln Phe Ile Arg His Gln Leu Leu Leu Arg Pro Glu Ser
 370 375 380
 Asp Asp Ser Ala Gln Leu Ser Gln Ile Glu Thr Glu Lys Leu Leu Ala
 385 390 395 400
 Gln Leu Val Glu Thr Glu Met Asn Lys Arg Leu Lys Glu Gly Thr Tyr
 405 410 415
 Lys Gly Lys Phe Asn Ala Ile Cys His Phe Phe Gly Tyr Gln Ala
 420 425 430
 Arg Gly Ala Met Pro Ser Lys Phe Asp Cys Asp Tyr Ala Tyr Val Leu
 435 440 445
 Gly His Val Ser Tyr His Ile Leu Ala Ala Gly Leu Asn Gly Tyr Met
 450 455 460
 Ala Thr Val Thr Asn Leu Lys Ser Pro Leu Asn Lys Trp Arg Cys Gly
 465 470 475 480
 Ala Ala Pro Ile Ser Ser Met Met Thr Val Lys Arg Trp Ser Arg Gly
 485 490 495
 Pro Ser Thr Thr Gln Ile Gly Lys Pro Ala Met His Met Ala Thr Val
 500 505 510
 Asp Leu Arg Gly Lys Ala Tyr Glu Leu Leu Arg Gln Asn Ser Ser Ser
 515 520 525
 Tyr Leu Leu Glu Asp Ile Tyr Arg Asn Pro Gly Pro Leu Gln Phe Glu
 530 535 540
 Gly Pro Gly Ala Asp Ser Lys Pro Ile Ser Leu Cys Val Glu Asp Gln
 545 550 555 560
 Asp Tyr Met Gly Arg Ile Lys Lys Leu Gln Glu Tyr Leu Glu Lys Val
 565 570 575
 Lys Ser Ile Val Lys Pro Gly Cys Ser Gln Asp Val Leu Lys Ala Ala
 580 585 590
 Leu Ser Ala Met Ser Ser Val Thr Glu Thr Leu Ala Ile Met Thr Ser
 595 600 605
 Ser Ser Thr Gly Gln Ala Pro Leu
 610 615

<210> 61

<211> 563

<212> PRT

<213> Lolium perenne

<400> 61
 Met Ala Ala Ala Ala Val Ala Thr Ser Asn Gly Ala Ser Ala Asn Gly
 1 5 10 15
 Pro Thr Pro Gly Arg Leu Ala Ser Val Tyr Ser Glu Val Gln Thr Ser
 20 25 30
 Arg Ile Ala His Ala Leu Pro Leu Pro Ser Val Leu Arg Ser His Phe
 35 40 45
 Thr Leu Ala Asp Gly Ala Ala Ser Ser Ala Thr Gly Asn Pro Glu Glu
 50 55 60
 Ile Ala Lys Leu Phe Pro Asn Leu Tyr Gly Gln Pro Ser Ala Ala Val
 65 70 75 80
 Val Pro Ser Ala Gln Pro Val Ala Thr Lys Pro Leu Lys Ile Gly Val
 85 90 95
 Val Leu Ser Gly Gly Gln Ala Pro Gly Gly His Asn Val Ile Cys Gly
 100 105 110
 Ile Phe Asp Tyr Leu Gln Glu Arg Ala Lys Gly Ser Thr Met Tyr Gly
 115 120 125
 Phe Lys Gly Gly Pro Ala Gly Val Met Lys Gly Lys Tyr Val Glu Leu
 130 135 140
 Asn Ala Asp Phe Val Tyr Pro Tyr Arg Asn Gln Gly Gly Phe Asp Met
 145 150 155 160
 Ile Cys Ser Gly Arg Asp Lys Ile Glu Thr Pro Glu Gln Phe Lys Gln
 165 170 175
 Ala Glu Asp Thr Val Thr Lys Leu Asp Leu Asp Gly Leu Val Val Ile
 180 185 190
 Gly Gly Asp Asp Ser Asn Thr Asn Ala Cys Leu Leu Gly Glu Tyr Phe
 195 200 205
 Arg Gly Arg Asn Leu Lys Thr Arg Val Ile Gly Cys Pro Lys Thr Ile
 210 215 220
 Asp Gly Asp Leu Lys Cys Lys Glu Val Pro Thr Ser Phe Gly Phe Asp
 225 230 235 240
 Thr Ala Cys Lys Ile Tyr Ser Glu Met Ile Gly Asn Val Met Thr Asp
 245 250 255
 Ala Arg Ser Thr Gly Lys Tyr Tyr His Phe Val Arg Leu Met Gly Arg
 260 265 270
 Ala Ala Ser His Ile Thr Leu Glu Cys Ala Leu Gln Thr His Pro Asn
 275 280 285
 Val Ser Leu Ile Gly Glu Glu Val Ala Glu Lys Lys Glu Thr Leu Lys
 290 295 300
 Gln Val Thr Asp Tyr Ile Thr Asp Val Ile Cys Lys Arg Ala Glu Leu
 305 310 315 320
 Gly Tyr Asn Tyr Gly Val Ile Leu Ile Pro Glu Gly Leu Ile Asp Phe
 325 330 335
 Ile Pro Glu Val Gln Lys Leu Ile Ala Glu Leu Asn Glu Ile Leu Ala
 340 345 350
 His Asp Val Val Asp Glu Ala Gly Ala Trp Lys Ser Lys Leu Gln Pro
 355 360 365
 Glu Ser Arg Gln Leu Phe Asp Phe Leu Pro Asn Thr Ile Gln Glu Gln
 370 375 380
 Leu Leu Leu Glu Arg Asp Pro His Gly Asn Val Gln Val Ala Lys Ile
 385 390 395 400
 Glu Thr Glu Lys Met Leu Ile Ala Met Val Glu Thr Glu Leu Glu Lys
 405 410 415
 Arg Arg Ser Ala Gly Lys Tyr Ser Ala His Phe Arg Gly Gln Ser His
 420 425 430
 Phe Phe Gly Tyr Glu Gly Arg Cys Gly Leu Pro Thr Asn Phe Asp Ser
 435 440 445
 Ser Tyr Cys Tyr Ala Leu Gly Tyr Gly Ala Gly Ala Leu Leu Gln Phe
 450 455 460
 Gly Lys Thr Gly Leu Ile Ser Ser Val Gly Asn Leu Ala Ala Pro Val
 465 470 475 480
 Glu Glu Trp Thr Val Gly Gly Thr Pro Leu Thr Ala Leu Met Asp Val
 485 490 495
 Glu Arg Arg His Gly Lys Phe Lys Pro Val Ile Lys Lys Ala Met Val
 500 505 510
 Glu Leu Asp Ala Ala Pro Phe Lys Lys Phe Ala Ser Met Arg Asp Glu
 515 520 525
 Trp Ala Ile Lys Asn Arg Tyr Ile Ser Pro Gly Pro Ile Gln Phe Ser

Gly	530	Pro	Gly	Ser	Asp	Ala	535	Ser	Asn	His	Thr	Leu	540	Met	Leu	Glu	Leu	Gly
	545					550						555						560
Ala		Gln		Thr														

<210> 62
<211> 563
<212> PRT
<213> *Lolium perenne*

<400> 62	Met Ala Ala Ala Ala Val Ala Thr Ser Asn Gly Ala Ser Ala Asn Gly	1	5	10	15
Pro Thr Pro Gly Arg Leu Ala Ser Val Tyr Ser Glu Val Gln Thr Ser	20	25	30		
Arg Ile Ala His Ala Leu Pro Leu Pro Ser Val Leu Arg Ser His Phe	35	40	45		
Thr Leu Ala Asp Gly Ala Ala Ser Ser Ala Thr Gly Asn Pro Glu Glu	50	55	60		
Ile Ala Lys Leu Phe Pro Asn Leu Tyr Gly Gln Pro Ser Ala Ala Val	65	70	75	80	
Val Pro Ser Ala Gln Pro Val Ala Thr Lys Pro Leu Lys Ile Gly Val	85	90	95		
Val Leu Ser Gly Gly Gln Ala Pro Gly Gly His Asn Val Ile Cys Gly	100	105	110		
Ile Phe Asp Tyr Leu Gln Glu Arg Ala Lys Gly Ser Thr Met Tyr Gly	115	120	125		
Phe Lys Gly Gly Pro Ala Gly Val Met Lys Gly Lys Tyr Val Glu Leu	130	135	140		
Asn Ala Asp Phe Val Tyr Pro Tyr Arg Asn Gln Gly Gly Phe Asp Met	145	150	155	160	
Ile Cys Ser Gly Arg Asp Lys Ile Glu Thr Pro Glu Gln Phe Lys Gln	165	170	175		
Ala Glu Asp Thr Val Thr Lys Leu Asp Leu Asp Gly Leu Val Val Ile	180	185	190		
Gly Gly Asp Asp Ser Asn Thr Asn Ala Cys Leu Leu Gly Glu Tyr Phe	195	200	205		
Arg Gly Arg Asn Leu Lys Thr Arg Val Ile Gly Cys Pro Lys Thr Ile	210	215	220		
Asp Gly Asp Leu Lys Cys Lys Glu Val Pro Thr Ser Phe Gly Phe Asp	225	230	235	240	
Thr Ala Cys Lys Ile Tyr Ser Glu Met Ile Gly Asn Val Met Thr Asp	245	250	255		
Ala Arg Ser Thr Gly Lys Tyr Tyr His Phe Val Arg Leu Met Gly Arg	260	265	270		
Ala Ala Ser His Ile Thr Leu Gln Cys Ala Leu Gln Thr His Pro Asn	275	280	285		
Val Ser Leu Ile Gly Glu Glu Val Ala Glu Lys Lys Glu Thr Leu Lys	290	295	300		
Gln Val Thr Asp Tyr Ile Thr Asp Val Ile Cys Lys Arg Ala Glu Leu	305	310	315	320	
Gly Tyr Asn Tyr Gly Val Ile Leu Ile Pro Glu Gly Leu Ile Asp Phe	325	330	335		
Ile Pro Glu Val Gln Lys Leu Ile Ala Glu Leu Asn Glu Ile Leu Ala	340	345	350		
His Asp Val Val Asp Glu Ala Gly Ala Trp Lys Ser Lys Leu Gln Pro	355	360	365		
Glu Ser Arg Gln Leu Phe Asp Phe Leu Pro Asn Thr Ile Gln Glu Gln	370	375	380		
Leu Leu Leu Glu Arg Asp Pro His Gly Asn Val Gln Val Ala Lys Ile	385	390	395	400	
Glu Thr Glu Lys Met Leu Ile Ala Met Val Glu Thr Glu Leu Glu Lys	405	410	415		
Arg Arg Ser Ala Gly Lys Tyr Ser Ala His Phe Arg Gly Gln Ser His	420	425	430		
Phe Phe Gly Tyr Glu Gly Arg Cys Gly Leu Pro Thr Asn Phe Asp Ser	435	440	445		

Ser Tyr Cys Tyr Ala Leu Gly Tyr Gly Ala Gly Ala Leu Leu Gln Phe
 450 455 460
 Gly Lys Thr Gly Leu Ile Ser Ser Val Gly Asn Leu Ala Ala Pro Val
 465 470 475 480
 Glu Glu Trp Thr Val Gly Gly Thr Pro Leu Thr Ala Leu Met Asp Val
 485 490 495
 Glu Arg Arg His Gly Lys Phe Lys Pro Val Ile Lys Lys Ala Met Val
 500 505 510
 Glu Leu Asp Ala Ala Pro Phe Lys Lys Phe Ala Ser Met Arg Asp Glu
 515 520 525
 Trp Ala Ile Lys Asn Arg Tyr Ile Ser Pro Gly Pro Ile Gln Phe Ser
 530 535 540
 Gly Pro Gly Ser Asp Ala Ser Asn His Thr Leu Met Leu Glu Leu Gly
 545 550 555 560
 Ala Gln Thr

<210> 63
 <211> 563
 <212> PRT
 <213> Festuca arundinacea

<400> 63
 Met Ala Ala Ala Ala Val Ala Thr Ser Asn Gly Ala Ser Ala Asn Gly
 1 5 10 15
 Pro Thr Pro Gly Arg Leu Ala Ser Val Tyr Ser Glu Val Gln Thr Ser
 20 25 30
 Arg Ile Ala His Ala Leu Pro Leu Pro Ser Val Leu Arg Ser Asn Phe
 35 40 45
 Thr Leu Ala Asp Gly Pro Ala Ser Ser Ala Thr Gly Asn Pro Glu Glu
 50 55 60
 Ile Ala Lys Leu Phe Pro Asn Leu Tyr Gly Gln Pro Ser Ala Ala Val
 65 70 75 80
 Val Pro Ser Ala Glu Pro Val Pro Thr Lys Pro Leu Lys Ile Gly Val
 85 90 95
 Val Leu Ser Gly Gly Gln Ala Pro Gly Gly His Asn Val Ile Cys Gly
 100 105 110
 Ile Phe Asp Tyr Leu Gln Glu Arg Ala Lys Gly Ser Thr Met Tyr Gly
 115 120 125
 Phe Lys Gly Gly Pro Ala Gly Ile Met Lys Gly Lys Tyr Ile Glu Leu
 130 135 140
 Asn Ala Asp Phe Val Tyr Pro Tyr Arg Asn Gln Gly Gly Phe Asp Met
 145 150 155 160
 Ile Cys Ser Gly Arg Asp Lys Ile Glu Thr Pro Glu Gln Phe Lys Gln
 165 170 175
 Ala Glu Asp Thr Val Asn Lys Leu Asp Leu Asp Gly Leu Val Val Ile
 180 185 190
 Gly Gly Asp Asp Ser Asn Thr Asn Ala Cys Leu Leu Gly Glu Tyr Phe
 195 200 205
 Arg Gly Arg Asn Leu Lys Thr Arg Val Ile Gly Cys Pro Lys Thr Ile
 210 215 220
 Asp Gly Asp Leu Lys Cys Lys Glu Val Pro Ile Ser Phe Gly Phe Asp
 225 230 235 240
 Thr Ala Cys Lys Ile Tyr Ser Glu Met Ile Gly Asn Val Met Thr Asp
 245 250 255
 Ala Arg Ser Thr Gly Lys Tyr Tyr His Phe Val Arg Leu Met Gly Arg
 260 265 270
 Ala Ala Ser His Ile Thr Leu Glu Cys Ala Leu Gln Thr His Pro Asn
 275 280 285
 Val Ser Leu Ile Gly Glu Glu Val Ala Glu Lys Lys Glu Thr Leu Lys
 290 295 300
 Gln Val Thr Asp Tyr Ile Thr Asp Val Ile Cys Lys Arg Ala Glu Leu
 305 310 315 320
 Gly Tyr Asn Tyr Gly Val Ile Leu Ile Pro Glu Gly Leu Ile Asp Phe
 325 330 335
 Ile Pro Glu Val Gln Lys Leu Ile Ala Glu Leu Asn Glu Ile Leu Ala
 340 345 350
 His Asp Val Val Asp Glu Ala Gly Ala Trp Lys Ser Lys Leu Gln Pro

Glu	Ser	Arg	Gln	Leu	Phe	Asp	Phe	Leu	Pro	Asn	Thr	Ile	Gln	Glu	Gln
355							360								365
370							375								380
Leu	Leu	Leu	Glu	Arg	Asp	Pro	His	Gly	Asn	Val	Gln	Val	Ala	Lys	Ile
385							390								395
Glu	Thr	Glu	Lys	Met	Leu	Ile	Ala	Met	Val	Glu	Thr	Glu	Leu	Glu	Lys
															400
							405								415
Arg	Arg	Ala	Ala	Gly	Lys	Tyr	Ser	Ala	His	Phe	Arg	Gly	Gln	Ser	His
							420								430
Phe	Phe	Gly	Tyr	Glu	Gly	Arg	Cys	Gly	Leu	Pro	Thr	Asn	Phe	Asp	Ser
							435								445
Ser	Tyr	Cys	Tyr	Ala	Leu	Gly	Tyr	Gly	Ala	Gly	Ala	Leu	Leu	Gln	Phe
							450								460
Gly	Lys	Thr	Gly	Leu	Ile	Ser	Ser	Val	Gly	Asn	Leu	Ala	Ala	Pro	Val
							465								475
Glu	Glu	Trp	Thr	Val	Gly	Gly	Thr	Pro	Leu	Thr	Ala	Leu	Met	Asp	Val
							485								495
Glu	Arg	Arg	His	Gly	Lys	Phe	Lys	Pro	Val	Ile	Lys	Lys	Ala	Met	Val
							500								510
Glu	Leu	Asp	Ala	Ala	Pro	Phe	Lys	Lys	Phe	Ala	Ser	Met	Arg	Asp	Glu
							515								525
Trp	Ala	Ile	Lys	Asn	Arg	Tyr	Ile	Ser	Pro	Gly	Pro	Ile	Gln	Phe	Ser
							530								540
Gly	Pro	Gly	Ser	Asp	Ala	Ser	Asn	His	Thr	Leu	Met	Leu	Glu	Leu	Gly
							545								560
Ala	Gln	Ile													

<210> 64

<211> 964

<212> PRT

<213> Lolium perenne

<400> 64

Met	Val	Gly	Asn	Asp	Asn	Trp	Ile	Asn	Ser	Tyr	Leu	Asp	Ala	Ile	Leu
1							5			10					15
Asp	Ala	Gly	Lys	Ser	Ser	Ile	Gly	Gly	Asp	Arg	Pro	Ser	Leu	Leu	Leu
							20			25					30
Arg	Glu	Arg	Gly	His	Phe	Ser	Pro	Ala	Arg	Tyr	Phe	Val	Glu	Glu	Val
							35			40					45
Ile	Thr	Gly	Tyr	Asp	Glu	Thr	Asp	Leu	Tyr	Lys	Thr	Trp	Leu	Arg	Ala
							50			55					60
Asn	Ala	Met	Arg	Ser	Pro	Gln	Glu	Arg	Asn	Thr	Arg	Leu	Glu	Asn	Met
							65			70					80
Thr	Trp	Arg	Ile	Trp	Asn	Leu	Ala	Arg	Lys	Lys	Lys	Glu	Leu	Lys	
							85			90					95
Glu	Glu	Ala	Cys	Arg	Leu	Leu	Lys	Arg	His	Pro	Glu	Thr	Glu	Lys	Thr
							100			105					110
Arg	Thr	Asp	Ala	Thr	Ala	Asp	Met	Ser	Glu	Asp	Leu	Phe	Asp	Gly	Glu
							115			120					125
Lys	Gly	Glu	Asp	Ala	Gly	Asp	Pro	Ser	Val	Ala	Tyr	Gly	Asp	Ser	Thr
							130			135					140
Thr	Gly	Ser	Ser	Pro	Lys	Thr	Ser	Ser	Val	Asp	Lys	Leu	Tyr	Ile	Val
							145			150					160
Leu	Ile	Ser	Leu	His	Gly	Leu	Val	Arg	Gly	Glu	Asn	Met	Glu	Leu	Gly
							165			170					175
Arg	Asp	Ser	Asp	Thr	Gly	Gly	Gln	Val	Lys	Tyr	Val	Val	Glu	Phe	Ala
							180			185					190
Lys	Ala	Leu	Ser	Ser	Ser	Pro	Gly	Val	Tyr	Arg	Val	Asp	Leu	Thr	
							195			200					205
Arg	Gln	Ile	Val	Ala	Pro	Asn	Phe	Asp	Arg	Ser	Tyr	Gly	Glu	Pro	Glu
							210			215					220
Glu	Met	Leu	Val	Ser	Thr	Thr	Phe	Lys	Asn	Ser	Lys	His	Glu	Arg	Gly
							225			230					240
Val	Asn	Ser	Gly	Gly	Tyr	Ile	Ile	Arg	Ile	Pro	Phe	Gly	Pro	Lys	Asp
							245			250					255
Lys	Tyr	Leu	Ala	Lys	Glu	His	Met	Trp	Pro	Phe	Ile	Gln	Asp	Phe	Val
							260			265					270

Asp Gly Ala Leu Ser His Ile Leu Arg Met Ser Lys Thr Ile Gly Glu
 275 280 285
 Glu Ile Gly Cys Gly His Pro Val Trp Pro Ala Val Ile His Gly His
 290 295 300
 Tyr Ala Ser Ala Gly Val Ala Ala Ala Leu Leu Ser Gly Ala Leu Asn
 305 310 315 320
 Leu Pro Met Ala Phe Thr Gly His Phe Leu Gly Lys Asp Lys Leu Glu
 325 330 335 340
 Gly Leu Leu Lys Gln Gly Arg Gln Ser Arg Glu Gln Ile Asn Met Thr
 345 350 355
 Tyr Lys Ile Met Arg Arg Ile Glu Ala Glu Glu Leu Ser Leu Asp Ala
 360 365 370
 Ser Glu Ile Val Ile Ala Ser Thr Arg Gln Glu Ile Glu Glu Gln Trp
 375 380 385
 Asn Leu Tyr Asp Gly Phe Glu Val Ile Leu Ala Arg Lys Leu Arg Ala
 390 395 400
 Arg Val Lys Arg Gly Ala Asn Cys Tyr Gly Arg Tyr Met Pro Arg Met
 405 410 415
 Val Ile Ile Pro Pro Gly Val Glu Phe Gly His Val Val His Asp Phe
 420 425 430
 Asp Met Asp Gly Glu Glu Glu Asn His Gly Pro Ala Ser Glu Asp Pro
 435 440 445
 Pro Ile Trp Ser Gln Ile Met Arg Phe Phe Thr Asn Pro Arg Lys Pro
 450 455 460
 Met Ile Leu Ala Val Ala Arg Pro Tyr Pro Glu Lys Asn Ile Thr Ser
 465 470 475 480
 Leu Val Lys Ala Phe Gly Glu Cys Arg Pro Leu Arg Glu Leu Ala Asn
 485 490 495
 Leu Thr Leu Ile Met Gly Asn Arg Glu Ala Ile Ser Lys Met His Asn
 500 505 510
 Thr Ser Ala Ser Val Leu Thr Ser Val Leu Thr Leu Ile Asp Glu Tyr
 515 520 525
 Asp Leu Tyr Gly Gln Val Ala Tyr Pro Lys His His Lys His Ser Glu
 530 535 540
 Val Pro Asp Ile Tyr Arg Leu Ala Thr Arg Thr Lys Gly Ala Phe Val
 545 550 555 560
 Asn Val Ala Tyr Phe Glu Gln Phe Gly Val Thr Leu Ile Glu Ala Ala
 565 570 575
 Met Asn Gly Leu Pro Val Ile Ala Thr Lys Asn Gly Ala Pro Val Glu
 580 585 590
 Ile Asn Gln Val Leu Asn Asn Gly Leu Leu Val Asp Pro His Asp Gln
 595 600 605
 Asn Ala Ile Ala Asp Ala Leu Tyr Lys Leu Leu Ser Glu Lys Gln Leu
 610 615 620
 Trp Ser Arg Cys Arg Glu Asn Gly Leu Lys Asn Ile His Gln Phe Ser
 625 630 635 640
 Trp Pro Glu His Cys Lys Asn His Leu Ser Arg Ile Leu Thr Leu Gly
 645 650 655
 Ala Arg Ser Pro Ala Ile Gly Ser Lys Glu Glu Arg Ser Asn Ala Pro
 660 665 670
 Ile Ser Gly Arg Lys His Ile Ile Val Ile Ser Val Asp Ser Val Asn
 675 680 685
 Lys Glu Asp Leu Val Arg Ile Ile Arg Asn Ala Ile Glu Ala Ala His
 690 695 700
 Thr Gln Asn Thr Pro Ala Ser Thr Gly Phe Val Leu Ser Thr Ser Leu
 705 710 715 720
 Thr Leu Ser Glu Ile Cys Ser Leu Leu Val Ser Val Gly Met His Pro
 725 730 735
 Ala Gly Phe Asp Ala Phe Ile Cys Asn Ser Gly Ser Ser Ile Tyr Tyr
 740 745 750
 Pro Ser Tyr Ser Gly Asn Thr Pro Ser Ser Ser Lys Val Thr His Val
 755 760 765
 Ile Asp Gln Asn His Gln Ser His Ile Glu Tyr Arg Trp Gly Gly Glu
 770 775 780
 Gly Leu Arg Lys Tyr Leu Val Lys Trp Ala Thr Ser Val Val Glu Arg
 785 790 795 800
 Lys Gly Arg Ile Glu Arg Gln Met Ile Phe Glu Asp Ser Glu His Ser
 805 810 815

Ser Thr Tyr Cys Leu Ala Phe Lys Val Val Asn Pro Asn His Leu Pro
 820 825 830
 Pro Leu Lys Glu Leu Arg Lys Leu Met Arg Ile Gln Ser Leu Arg Cys
 835 840 845
 Asn Ala Leu Tyr Asn His Ser Ala Thr Arg Leu Ser Val Thr Pro Ile
 850 855 860
 His Ala Ser Arg Ser Gln Ala Ile Arg Tyr Leu Phe Ile Arg Trp Gly
 865 870 875 880
 Ile Glu Leu Pro Asn Ile Val Val Leu Val Gly Glu Ser Gly Asp Ser
 885 890 895
 Asp Tyr Glu Glu Leu Leu Gly Gly Leu His Arg Thr Ile Ile Leu Lys
 900 905 910
 Gly Asp Phe Asn Ile Ala Ala Asn Arg Ile His Thr Val Arg Arg Tyr
 915 920 925
 Pro Leu Gln Asp Val Val Ala Leu Asp Ser Ser Asn Ile Ile Glu Val
 930 935 940
 Glu Gly Cys Thr Thr Asp Val Ile Lys Ser Ala Leu Arg Gln Ile Gly
 945 950 955 960
 Val Pro Thr Gln

<210> 65
 <211> 984
 <212> PRT

<213> Festuca arundinacea

<220>
 <221> VARIANT
 <222> (1)...(984)
 <223> Xaa = Any Amino Acid

<400> 65
 Met Val Gly Gly Met Cys Gly Asn Asp Asn Trp Ile Asn Ser Tyr Leu
 1 5 10 15
 Asp Ala Ile Leu Asp Ala Gly Lys Gly Ala Pro Gly Gly Ala Gly
 20 25 30
 Pro Gly Gly Arg Gly Gly Gly Gly Gly Ala Gly Asp Arg Pro
 35 40 45
 Ser Leu Leu Leu Arg Glu Arg Gly His Phe Ser Pro Ala Arg Tyr Phe
 50 55 60
 Val Glu Glu Val Ile Thr Gly Tyr Asp Glu Thr Asp Leu Tyr Lys Thr
 65 70 75 80
 Trp Ser Arg Ala Asn Ala Met Arg Ser Pro Gln Glu Arg Asn Thr Arg
 85 90 95
 Leu Glu Asn Met Thr Trp Arg Ile Trp Asn Leu Ala Arg Lys Lys Lys
 100 105 110
 Glu Xaa Ala Glu Glu Ala Asn Arg Leu Leu Lys Arg Arg Leu Glu
 115 120 125
 Thr Glu Lys Pro Arg Thr Asp Ala Ala Ala Glu Met Ser Glu Asp Leu
 130 135 140
 Phe Glu Gly Gln Lys Gly Glu Asp Ala Gly Asp Ala Ser Val Ala Tyr
 145 150 155 160
 Gly Asp Ser Ser Ala Ser Asn Thr Pro Arg Ile Ser Ser Ile Asp Lys
 165 170 175
 Leu Tyr Ile Val Leu Ile Ser Leu His Gly Leu Val Arg Gly Glu Asn
 180 185 190
 Met Glu Leu Gly Arg Asp Ser Asp Thr Ser Gly Gln Val Lys Tyr Val
 195 200 205
 Val Glu Leu Ala Lys Ala Leu Ser Ser Cys Pro Gly Val Tyr Arg Val
 210 215 220
 Asp Leu Leu Thr Arg Gln Ile Leu Ala Pro Asn Tyr Asp Arg Gly Tyr
 225 230 235 240
 Gly Glu Pro Ser Glu Thr Leu Leu Pro Thr Asn Leu Lys Asn Phe Lys
 245 250 255
 His Glu Arg Gly Glu Asn Ser Gly Ala Tyr Ile Thr Arg Ile Pro Phe
 260 265 270
 Gly Pro Lys Asp Lys Tyr Leu Ala Lys Glu Gln Leu Trp Pro Tyr Val
 275 280 285

Gln Glu Phe Val Asp Gly Ala Leu Ser His Ile Val Arg Met Ser Lys
 290 295 300
 Thr Ile Gly Glu Glu Ile Gly Cys Gly His Pro Met Trp Pro Ala Ala
 305 310 315 320
 Ile His Gly His Tyr Ala Ser Ala Gly Val Ala Ala Ala Leu Ser
 325 330 335
 Gly Ala Leu Asn Val His Met Ile Phe Thr Gly His Phe Leu Gly Arg
 340 345 350 355
 Asp Lys Leu Glu Gly Leu Leu Lys Gln Gly Lys Gln Thr Arg Glu Glu
 355 360 365
 Ile Asn Met Thr Tyr Lys Ile Met Arg Arg Ile Glu Ala Glu Glu Leu
 370 375 380
 Ser Leu Asp Ala Ser Glu Ile Val Ile Ala Ser Thr Arg Gln Glu Ile
 385 390 395 400
 Glu Glu Gln Trp Asn Leu Tyr Asp Gly Phe Glu Val Met Leu Ala Arg
 405 410 415
 Lys Leu Arg Ala Arg Val Lys Arg Gly Ala Asn Cys Tyr Gly Arg Tyr
 420 425 430
 Met Pro Arg Met Val Ile Ile Pro Pro Gly Val Glu Phe Gly His Met
 435 440 445
 Ile Gln Asp Phe Asp Met Asp Gly Glu Glu Asp Ser Pro Ser Pro Ala
 450 455 460
 Ser Glu Asp Pro Pro Ile Trp Ser Glu Ile Met Arg Phe Phe Thr Asn
 465 470 475 480
 Pro Arg Lys Pro Leu Ile Leu Ala Val Ala Arg Pro Tyr Pro Glu Lys
 485 490 495
 Asn Ile Thr Thr Leu Val Arg Ala Phe Gly Glu Cys Arg Pro Leu Arg
 500 505 510
 Glu Leu Ala Asn Leu Thr Leu Ile Met Gly Asn Arg Glu Ala Ile ser
 515 520 525
 Lys Met Ser Asn Met Ser Ala Ala Val Leu Thr Ser Val Leu Thr Leu
 530 535 540
 Ile Asp Glu Tyr Asp Leu Tyr Gly Gln Val Ala Tyr Pro Lys His His
 545 550 555 560
 Lys His Ser Glu Val Leu Asp Ile Tyr Arg Leu Ala Ala Arg Thr Lys
 565 570 575
 Gly Ala Phe Val Asn Val Ala Tyr Phe Glu Gln Phe Gly Val Thr Leu
 580 585 590
 Ile Glu Ala Ala Met His Gly Leu Pro Val Ile Ala Thr Lys Asn Gly
 595 600 605
 Ala Pro Val Glu Ile His Gln Val Leu Asn Asn Gly Leu Leu Val Asp
 610 615 620
 Pro His Asp Gln Asn Ala Ile Ala Asp Ala Leu Tyr Lys Leu Leu Ser
 625 630 635 640
 Glu Lys Gln Leu Trp Ser Arg Cys Arg Glu Asn Gly Leu Lys Asn Ile
 645 650 655
 His Gln Phe Ser Trp Pro Glu His Cys Lys Asn Tyr Leu Ser Arg Ile
 660 665 670
 Leu Thr Leu Ser Pro Arg Tyr Pro Ala Phe Ala Ser Asn Asp Asp Gln
 675 680 685
 Ile Lys Ala Pro Ile Lys Gly Arg Lys Tyr Ile Ile Val Ile Ala Val
 690 695 700
 Asp Ser Ala Ser Lys Lys Asp Leu Ala Phe Ile Ile Arg Asn Ser Ile
 705 710 715 720
 Glu Ala Thr Arg Thr Glu Thr Ser Ser Gly Ser Thr Gly Phe Val Leu
 725 730 735
 Ser Thr Ser Leu Thr Ile Ser Glu Ile His Ser Leu Leu Ile Ser Ala
 740 745 750
 Gly Met Val Pro Thr Asp Phe Asp Ala Phe Ile Cys Asn Ser Gly Ser
 755 760 765
 Asp Leu Phe Tyr Pro Ser Gln Thr Gly Asp Ser Pro Ser Thr Ser Arg
 770 775 780
 Val Thr Phe Ala Leu Asp Arg Asn Tyr Gln Ser Arg Val Glu Tyr His
 785 790 795 800
 Trp Gly Gly Glu Gly Leu Arg Lys Tyr Leu Val Lys Trp Ala Ser Ser
 805 810 815
 Val Val Glu Arg Arg Gly Arg Met Glu Lys Gln Val Ile Phe Asp Asp
 820 825 830

Ser Glu His Ser Ser Thr Cys Cys Leu Ala Phe Arg Val Val Asn Pro
 835 840 845
 Asn Tyr Leu Pro Pro Leu Lys Glu Leu Gln Lys Leu Met Arg Val Gln
 850 855 860
 Ser Leu Arg Cys His Ala Leu Tyr Asn His Ser Ala Thr Arg Leu Ser
 865 870 875 880
 Val Ile Pro Ile His Ala Ser Arg Ser Gln Ala Ile Arg Tyr Leu Ser
 885 890 895
 Val Arg Trp Gly Ile Glu Leu Pro Asn Val Val Ile Leu Val Gly Glu
 900 905 910
 Ser Gly Asp Ser Asp Tyr Glu Glu Leu Phe Gly Gly Leu His Lys Thr
 915 920 925
 Val Val Leu Asn Gly Glu Phe Asn Thr Pro Ala Asn Arg Ile His Thr
 930 935 940
 Val Arg Arg Tyr Pro Leu Gln Asp Val Ile Ala Leu Asp Cys Ser Asn
 945 950 955 960
 Ile Val Gly Val Gln Gly Cys Ser Thr Asp Cys Met Arg Ser Thr Leu
 965 970 975
 Glu Lys Leu Gly Ile Pro Thr Lys
 980

<210> 66
 <211> 522
 <212> PRT

<213> Festuca arundinacea

<400> 66
 Met Val Arg Gly Gly Asn Gly Glu Val Glu Leu Ser Val Gly Ala
 1 5 10 15
 Gly Gly Gly Gly Gly Ala Gly Gly Leu Val Glu Pro Pro Val Pro
 20 25 30
 Ile Ser Leu Gly Arg Leu Val Leu Ala Gly Met Val Ala Gly Gly Val
 35 40 45
 Gln Tyr Gly Trp Ala Leu Gln Leu Ser Leu Leu Thr Pro Tyr Val Gln
 50 55 60
 Thr Leu Gly Leu Ser His Ala Leu Thr Ser Phe Met Trp Leu Cys Gly
 65 70 75 80
 Pro Ile Ala Gly Leu Val Val Gln Pro Cys Val Gly Leu Tyr Ser Asp
 85 90 95
 Lys Cys Thr Ser Arg Trp Gly Arg Arg Pro Phe Ile Met Thr Gly
 100 105 110
 Cys Val Leu Ile Cys Ile Ala Val Val Ile Val Gly Phe Ser Ala Asp
 115 120 125
 Ile Gly Ala Ala Leu Gly Asp Ser Lys Glu Glu Cys Ser Leu Tyr His
 130 135 140
 Gly Pro Arg Trp His Ala Ala Ile Val Tyr Val Leu Gly Phe Trp Leu
 145 150 155 160
 Leu Asp Phe Ser Asn Asn Thr Val Gln Gly Pro Ala Arg Ala Leu Met
 165 170 175
 Ala Asp Leu Ser Gly Lys Tyr Gly Pro Ser Ala Ala Asn Ser Ile Phe
 180 185 190
 Cys Ser Trp Met Ala Leu Gly Asn Ile Leu Gly Tyr Ser Ser Gly Ser
 195 200 205
 Thr Asp Lys Trp His Lys Trp Phe Pro Phe Leu Arg Thr Arg Ala Cys
 210 215 220
 Cys Glu Ala Cys Ala Asn Leu Lys Gly Ala Phe Leu Val Ala Val Leu
 225 230 235 240
 Phe Leu Cys Met Cys Leu Val Ile Thr Leu Ile Phe Ala Lys Glu Val
 245 250 255
 Pro Tyr Lys Arg Ile Ala Pro Leu Pro Thr Lys Ala Asn Gly Gln Val
 260 265 270
 Glu Val Glu Pro Ser Gly Pro Leu Ala Val Phe Gln Gly Ile Arg Asn
 275 280 285
 Leu Pro Ser Gly Met Pro Ser Val Leu Leu Val Thr Gly Leu Thr Trp
 290 295 300
 Leu Ser Trp Phe Pro Phe Ile Leu Tyr Asp Thr Asp Trp Met Gly Arg
 305 310 315 320
 Glu Ile Tyr His Gly Asp Pro Lys Gly Thr Pro Ala Glu Met Ser Ala

Phe	Gln	Asp	Gly	Val	Arg	Ala	Gly	Ala	Phe	Gly	Leu	Leu	Leu	Asn	Ser
325							330							335	
340							345							350	
Ile	Ile	Leu	Gly	Phe	Ser	Ser	Phe	Leu	Ile	Glu	Pro	Met	Cys	Lys	Arg
355							360							365	
Leu	Gly	Pro	Arg	Val	Val	Trp	Val	Ser	Ser	Asn	Phe	Leu	Val	Cys	Ile
370						375								380	
Ala	Met	Ala	Ala	Thr	Ala	Ile	Ile	Ser	Trp	Trp	Ser	Thr	Lys	Glu	Phe
385						390								400	
His	Glu	Tyr	Val	Gln	His	Ala	Ile	Thr	Ala	Ser	Lys	Asp	Ile	Lys	Ile
														415	
Val	Cys	Met	Ala	Leu	Phe	Ala	Phe	Leu	Gly	Val	Pro	Leu	Ala	Ile	Leu
														420	
Tyr	Ser	Val	Pro	Phe	Ala	Val	Thr	Ala	Gln	Leu	Ala	Ala	Ser	Lys	Gly
														425	
Gly	Gly	Gly	Gly	Leu	Cys	Thr	Gly	Val	Leu	Asn	Ile	Ser	Ile	Val	Ile
														430	
Pro	Gln	Val	Ile	Ile	Ala	Leu	Gly	Ala	Gly	Pro	Trp	Asp	Gln	Leu	Phe
														435	
Gly	Lys	Gly	Asn	Ile	Pro	Ala	Phe	Ala	Ala	Ala	Ser	Ala	Phe	Ala	Leu
														440	
Ile	Gly	Gly	Ile	Val	Gly	Ile	Phe	Leu	Leu	Pro	Lys	Ile	Ser	Arg	Arg
														445	
Ser	Phe	Arg	Ala	Val	Ser	Thr	Gly	Gly	His						450
														455	
														460	
														465	
														470	
														475	
														480	
														485	
														490	
														495	
														500	
														505	
														510	
														515	

<210> 67
<211> 407
<212> PRT
<213> Festuca arundinacea

<400>	67														
Ile	Cys	Val	Ala	Val	Val	Val	Val	Gly	Phe	Ser	Ala	Asp	Ile	Gly	Ala
1								5					10		15
Ala	Leu	Gly	Asp	Ser	Lys	Glu	Glu	Cys	Ser	Leu	Tyr	His	Gly	Pro	Arg
								20					25		30
Trp	His	Ala	Ala	Ile	Val	Tyr	Val	Leu	Gly	Phe	Trp	Leu	Leu	Asp	Phe
								35					40		45
Ser	Asn	Asn	Thr	Val	Gln	Gly	Pro	Ala	Arg	Ala	Leu	Met	Ala	Asp	Leu
								50					55		60
Ser	Gly	Lys	Tyr	Gly	Pro	Ser	Ala	Ala	Asn	Ile	Phe	Cys	Ser	Trp	
								65					70		75
Met	Ala	Leu	Gly	Asn	Ile	Leu	Gly	Tyr	Ser	Ser	Gly	Ser	Thr	Asp	Lys
								85					90		95
Trp	His	Lys	Trp	Phé	Pro	Phe	Leu	Arg	Thr	Arg	Ala	Cys	Cys	Glu	Ala
								100					105		110
Cys	Ala	Asn	Leu	Lys	Gly	Ala	Phe	Leu	Val	Ala	Val	Leu	Phe	Leu	Cys
								115					120		125
Phe	Cys	Leu	Val	Ile	Thr	Leu	Ile	Phe	Ala	Lys	Glu	Val	Pro	Tyr	Lys
								130					135		140
Arg	Ile	Ala	Pro	Leu	Pro	Thr	Lys	Ala	Asn	Gly	Gln	Val	Glu	Val	Glu
								145					150		155
Pro	Ser	Gly	Pro	Leu	Ala	Val	Phe	Gln	Gly	Phe	Arg	Asn	Leu	Pro	Ser
								165					170		175
Gly	Met	Pro	Ser	Val	Leu	Leu	Val	Thr	Gly	Leu	Thr	Trp	Leu	Ser	Trp
								180					185		190
Phe	Pro	Phe	Ile	Leu	Tyr	Asp	Thr	Asp	Trp	Met	Gly	Arg	Glu	Ile	Tyr
								195					200		205
His	Gly	Asp	Pro	Lys	Gly	Thr	Pro	Ala	Glu	Ala	Ser	Ala	Phe	Gln	Asp
								210					215		220
Gly	Val	Arg	Ala	Gly	Ala	Phe	Gly	Leu	Leu	Leu	Asn	Ser	Ile	Ile	Leu
								225					230		235
Gly	Phe	Ser	Ser	Phe	Leu	Ile	Glu	Pro	Met	Cys	Lys	Arg	Leu	Gly	Pro
								245					250		255
Arg	Val	Val	Trp	Val	Ser	Ser	Asn	Leu	Leu	Val	Cys	Ile	Ala	Met	Ala
								260					265		270
Ala	Thr	Ala	Ile	Ile	Ser	Trp	Trp	Ser	Thr	Lys	Glu	Phe	His	Glu	Tyr
								275					280		285

Val Gln His Ala Ile Thr Ala Ser Lys Asp Ile Lys Ile Val Cys Met
 290 295 300
 Val Leu Phe Ala Phe Leu Gly Val Pro Leu Ala Ile Leu Tyr Ser Val
 305 310 315 320
 Pro Phe Ala Val Thr Ala Gln Leu Ala Ala Asn Lys Gly Gly Gln
 325 330 335
 Gly Leu Cys Thr Gly Val Leu Asn Ile Ser Ile Val Ile Pro Gln Val
 340 345 350
 Ile Ile Ala Leu Gly Ala Gly Pro Trp Asp Gln Leu Phe Gly Lys Gly
 355 360 365
 Asn Ile Pro Ala Phe Ala Ala Ser Ala Phe Ala Leu Ile Gly Gly
 370 375 380
 Ile Val Gly Ile Phe Leu Leu Pro Lys Ile Ser Arg His Ser Phe Arg
 385 390 395 400
 Ala Val Ser Thr Gly Gly His
 405

<210> 68

<211> 522

<212> PRT

<213> Festuca arundinacea

<400> 68

Met Val Arg Gly Gly Gly Asn Ser Glu Val Glu Leu Ser Val Gly Ala
 1 5 10 15
 Gly Gly Gly Gly Gly Ala Gly Gly Leu Val Glu Pro Pro Val Pro
 20 25 30
 Ile Ser Leu Gly Arg Leu Val Phe Ala Gly Met Val Ala Gly Gly Val
 35 40 45
 Gln Tyr Gly Trp Ala Leu Gln Leu Ser Leu Leu Thr Pro Tyr Val Gln
 50 55 60
 Thr Leu Gly Leu Ser His Ala Leu Thr Ser Phe Met Trp Leu Cys Gly
 65 70 75 80
 Pro Ile Ala Gly Leu Val Val Gln Pro Cys Val Gly Leu Tyr Ser Asp
 85 90 95
 Lys Cys Thr Ser Arg Trp Gly Arg Arg Pro Phe Ile Met Thr Gly
 100 105 110
 Cys Val Leu Ile Cys Ile Ala Val Val Ile Val Gly Phe Ser Ala Asp
 115 120 125
 Ile Gly Ala Ala Leu Gly Asp Ser Lys Glu Glu Cys Ser Leu Tyr His
 130 135 140
 Gly Pro Arg Trp His Ala Ala Ile Val Tyr Val Leu Gly Phe Trp Leu
 145 150 155 160
 Leu Asp Phe Ser Asn Asn Thr Val Gln Gly Pro Ala Arg Ala Leu Met
 165 170 175
 Ala Asp Leu Ser Gly Lys Tyr Gly Pro Ser Ala Ala Asn Ser Ile Phe
 180 185 190
 Cys Ser Trp Met Ala Leu Gly Asn Ile Leu Gly Tyr Ser Ser Gly Ser
 195 200 205
 Thr Asp Lys Trp His Lys Trp Phe Pro Phe Leu Arg Thr Arg Ala Cys
 210 215 220
 Cys Glu Ala Cys Ala Asn Leu Lys Gly Ala Phe Leu Val Ala Val Leu
 225 230 235 240
 Phe Leu Cys Phe Cys Leu Val Ile Thr Leu Ile Phe Ala Lys Glu Val
 245 250 255
 Pro Tyr Lys Arg Ile Ala Pro Leu Pro Thr Lys Ala Asn Gly Gln Val
 260 265 270
 Glu Val Glu Pro Ser Gly Pro Leu Ala Val Phe Gln Gly Phe Arg Asn
 275 280 285
 Leu Pro Ser Gly Met Pro Ser Val Leu Leu Val Thr Gly Leu Thr Trp
 290 295 300
 Leu Ser Trp Phe Pro Phe Ile Leu Tyr Asp Thr Asp Trp Met Gly Arg
 305 310 315 320
 Glu Ile Tyr His Gly Asp Pro Lys Gly Thr Pro Ala Glu Ala Ser Ala
 325 330 335
 Phe Gln Asp Gly Val Arg Ala Gly Ala Phe Gly Leu Leu Leu Asn Ser
 340 345 350
 Ile Ile Leu Gly Phe Ser Ser Phe Leu Ile Glu Pro Met Cys Lys Arg

Leu Gly Pro Arg Val Val Trp Val Ser Ser Asn Leu Leu Val Cys Ile
 355 360 365
 370 375 380
 Ala Met Ala Ala Thr Ala Ile Ile Ser Trp Trp Ser Thr Lys Glu Phe
 385 390 395 400
 His Glu Tyr Val Gln His Ala Ile Thr Ala Ser Lys Asp Ile Lys Ile
 405 410 415
 Val Cys Met Val Leu Phe Ala Phe Leu Gly Val Pro Leu Ala Ile Leu
 420 425 430
 Tyr Ser Val Pro Phe Ala Val Thr Ala Gln Leu Ala Ala Asn Lys Gly
 435 440 445
 Gly Gly Gln Gly Leu Cys Thr Gly Val Leu Asn Ile Ser Ile Val Ile
 450 455 460
 Pro Gln Val Ile Ile Ala Leu Gly Ala Gly Pro Trp Asp Gln Leu Phe
 465 470 475 480
 Gly Lys Gly Asn Ile Pro Ala Phe Ala Ala Ser Ala Phe Ala Leu
 485 490 495
 Ile Gly Gly Ile Val Gly Ile Phe Leu Leu Pro Lys Ile Ser Arg His
 500 505 510
 Ser Phe Arg Ala Val Ser Thr Gly Gly His
 515 520

<210> 69

<211> 506

<212> PRT

<213> Lolium perenne

<400> 69

Met Pro Pro Pro Arg Arg Pro Thr Thr Gly Gly Thr Thr Thr Ser
 1 5 10 15
 Ala Ala Leu Pro Pro Pro Arg Lys Val Pro Leu Arg Ser Leu Leu Arg
 20 25 30
 Ala Ala Ser Val Ala Cys Gly Val Gln Phe Gly Trp Ala Leu Gln Leu
 35 40 45
 Ser Leu Leu Thr Pro Tyr Val Gln Glu Leu Gly Ile Pro His Ala Phe
 50 55 60
 Ala Ser Leu Val Trp Leu Cys Gly Pro Leu Ser Gly Leu Leu Val Gln
 65 70 75 80
 Pro Leu Ile Gly His Leu Ser Asp Arg Ile Ala Pro Ala Asp Ser Pro
 85 90 95
 Leu Gly Arg Arg Arg Pro Phe Ile Ala Ala Gly Ala Ala Ser Ile Ala
 100 105 110
 Phe Ser Val Leu Thr Val Gly Phe Ser Ala Asp Leu Gly Arg Leu Phe
 115 120 125
 Gly Asp Asn Val Arg Pro Gly Ser Thr Arg Tyr Gly Ala Ile Ile Val
 130 135 140
 Tyr Met Ile Gly Phe Trp Leu Leu Asp Val Gly Asn Asn Ala Thr Gln
 145 150 155 160
 Gly Pro Cys Arg Ala Phe Leu Ala Asp Leu Thr Glu Asn Asp Pro Arg
 165 170 175
 Arg Thr Arg Ile Ala Asn Ala Tyr Phe Ser Leu Phe Met Ala Leu Gly
 180 185 190
 Asn Ile Leu Gly Tyr Ala Thr Gly Ala Tyr Ser Gly Trp Tyr Lys Ile
 195 200 205
 Phe Pro Phe Thr Ile Thr Glu Ser Cys Gly Val Ser Cys Ala Asn Leu
 210 215 220
 Lys Ser Ala Phe Leu Leu Asp Ile Ile Ile Leu Ala Ile Thr Thr Tyr
 225 230 235 240
 Val Thr Val Val Thr Val Gln Asp Asn Pro Thr Phe Gly Ser Asp Glu
 245 250 255
 Ala Ala Pro Arg Pro Ser Ser His Glu Glu Glu Ala Phe Leu Phe Glu
 260 265 270
 Leu Phe Gly Ser Phe Lys Tyr Phe Thr Met Pro Val Trp Met Val Leu
 275 280 285
 Ile Val Thr Ser Leu Thr Trp Ile Gly Trp Phe Pro Phe Ile Leu Phe
 290 295 300
 Asp Thr Asp Trp Met Gly Arg Glu Ile Tyr Arg Gly Ser Pro Glu Ile
 305 310 315 320

Val Ala Asp Thr Gln Lys Tyr His Asp Gly Val Arg Met Gly Ser Phe
 325 330 335
 Gly Leu Met Leu Asn Ser Val Leu Leu Gly Ile Thr Ser Val Val Thr
 340 345 350
 Glu Lys Leu Cys Arg Lys Trp Gly Ala Gly Leu Val Trp Gly Val Ser
 355 360 365
 Asn Ile Ile Met Ala Leu Cys Phe Val Ala Met Leu Val Ile Thr Tyr
 370 375 380
 Val Ala Gln Asn Leu Asp Tyr Gly Pro Ser Gly Ala Pro Pro Thr Gly
 385 390 395 400
 Ile Val Val Ala Ser Leu Thr Val Phe Thr Ile Leu Gly Ala Pro Leu
 405 410 415
 Ser Ile Thr Tyr Ser Ile Pro Tyr Ala Met Ala Thr Ser Arg Val Glu
 420 425 430
 Asn Leu Gly Leu Gly Gln Gly Leu Ala Met Gly Ile Leu Asn Leu Ser
 435 440 445
 Ile Val Ile Pro Gln Ile Ile Val Ser Leu Gly Ser Gly Pro Trp Asp
 450 455 460
 Ser Leu Phe Gly Gly Asn Ala Pro Ser Phe Trp Val Ala Ala Ala
 465 470 475 480
 Ala Ser Phe Ile Gly Gly Leu Val Ala Ile Leu Gly Leu Pro Arg Ala
 485 490 495
 Arg Ile Ala Pro Lys Lys Arg Ser Gln Arg
 500 505

<210> 70

<211> 504

<212> PRT

<213> Festuca arundinacea

<400> 70
 Met Pro Pro Pro Arg Arg Pro Asn Ala Gly Gly Thr Thr Ser Ala Pro
 1 5 10 15
 Leu Pro Pro Pro Arg Lys Val Pro Leu Arg Ser Leu Leu Arg Ala Ala
 20 25 30
 Ser Val Ala Cys Gly Val Gln Phe Gly Trp Ala Leu Gln Leu Ser Leu
 35 40 45
 Leu Thr Pro Tyr Val Gln Glu Leu Gly Ile Pro His Ala Phe Ala Ser
 50 55 60
 Leu Val Trp Leu Cys Gly Pro Leu Ser Gly Leu Leu Val Gln Pro Leu
 65 70 75 80
 Ile Gly His Leu Ser Asp Arg Ile Ala Pro Ala Asp Ser Pro Leu Gly
 85 90 95
 Arg Arg Arg Pro Phe Ile Ala Ala Gly Ala Ala Ser Ile Ala Phe Ser
 100 105 110
 Val Leu Thr Val Gly Phe Ser Ala Asp Leu Gly Arg Leu Phe Gly Asp
 115 120 125
 Asn Ile Arg Pro Gly Ser Thr Arg Phe Gly Ala Ile Ile Val Tyr Met
 130 135 140
 Ile Gly Phe Trp Leu Leu Asp Val Gly Asn Asn Ala Thr Gln Gly Pro
 145 150 155 160
 Cys Arg Ala Phe Leu Ala Asp Leu Thr Glu Asn Asp Pro Arg Arg Thr
 165 170 175
 Arg Ile Ala Asn Ala Tyr Phe Ser Leu Phe Met Ala Leu Gly Asn Ile
 180 185 190
 Leu Gly Tyr Ala Thr Gly Ala Tyr Ser Gly Trp Tyr Lys Ile Phe Pro
 195 200 205
 Phe Thr Ile Thr Glu Ser Cys Gly Val Ser Cys Ala Asn Leu Lys Ser
 210 215 220
 Ala Phe Leu Leu Asp Ile Ile Leu Ala Ile Thr Thr Tyr Val Thr
 225 230 235 240
 Val Val Thr Val Gln Asp Asn Pro Thr Phe Gly Ser Asp Glu Ala Ala
 245 250 255
 Pro Arg Pro Ser Ser His Glu Glu Ala Phe Leu Phe Glu Leu Phe
 260 265 270
 Gly Ser Phe Lys Tyr Phe Thr Leu Pro Val Trp Met Val Leu Ile Val
 275 280 285
 Thr Ser Leu Thr Trp Ile Gly Trp Phe Pro Phe Ile Leu Phe Asp Thr

Asp	Trp	Met	Gly	Arg	Glu	Ile	Tyr	Arg	Gly	Ser	Pro	Glu	Ile	Val	Ala
305					310				315						320
Asp	Thr	Gln	Lys	Tyr	His	Asp	Gly	Val	Arg	Met	Gly	Ser	Phe	Gly	Leu
					325				330						335
Met	Leu	Asn	Ser	Val	Leu	Leu	Gly	Ile	Thr	Ser	Val	Val	Met	Glu	Lys
					340				345						350
Leu	Cys	Arg	Lys	Trp	Gly	Ala	Gly	Leu	Val	Trp	Gly	Val	Ser	Asn	Ile
					355				360						365
Ile	Met	Ala	Leu	Cys	Phe	Val	Ala	Met	Leu	Ile	Ile	Thr	Tyr	Val	Ala
					370				375						380
Lys	Asn	Leu	Asp	Tyr	Gly	Pro	Ser	Gly	Ala	Pro	Pro	Thr	Gly	Ile	Val
					385				390						400
Val	Ala	Ser	Leu	Ala	Val	Phe	Thr	Ile	Leu	Gly	Ala	Pro	Leu	Ser	Ile
					405				410						415
Thr	Tyr	Ser	Ile	Pro	Tyr	Ala	Met	Ala	Thr	Ser	Arg	Val	Glu	Asn	Leu
					420				425						430
Gly	Leu	Gly	Gln	Gly	Leu	Ala	Met	Gly	Ile	Leu	Asn	Leu	Ser	Ile	Val
					435				440						445
Ile	Pro	Gln	Ile	Ile	Val	Ser	Leu	Gly	Ser	Gly	Pro	Trp	Asp	Ser	Leu
					450				455						460
Phe	Gly	Gly	Gly	Asn	Ala	Pro	Ser	Phe	Trp	Val	Ala	Ala	Ala	Ser	
					465				470						480
Phe	Ile	Gly	Gly	Leu	Val	Ala	Ile	Leu	Gly	Leu	Pro	Arg	Ala	Arg	Ile
					485				490						495
Ala	Pro	Lys	Lys	Arg	Ser	Gln	Arg								
					500										

<210> 71

<211> 508

<212> PRT

<213> Lolium perenne

<400> 71

Met	Val	Asp	Gln	Asp	His	Asp	Gly	Arg	Arg	Arg	Gln	Glu	Glu	Ala	Thr
1					5				10						15
Ala	Val	Ala	Ala	Ser	Ser	Val	Pro	Leu	Leu	Glu	Lys	Lys	Pro	Gly	Asp
					20				25						30
Val	Pro	Tyr	Tyr	Val	Glu	Gly	Cys	Pro	Gly	Cys	Ala	Val	Asp	Arg	Arg
					35				40						45
Lys	Ala	Thr	Asp	Pro	Gly	Ile	Pro	Tyr	Gly	Ser	Phe	Ile	Tyr	Ile	Trp
					50				55						60
Val	Val	Ile	Leu	Cys	Thr	Ala	Ile	Pro	Ile	Ser	Ser	Leu	Phe	Pro	Phe
					65				70						80
Leu	Tyr	Phe	Met	Ile	Arg	Asp	Leu	His	Ile	Ala	Glu	Arg	Thr	Glu	Asp
					85				90						95
Ile	Gly	Phe	Tyr	Ala	Gly	Phe	Val	Gly	Ala	Ala	Phe	Met	Phe	Gly	Arg
					100				105						110
Cys	Leu	Thr	Ser	Thr	Ile	Trp	Gly	Ile	Ala	Ala	Asp	Arg	Ile	Gly	Arg
					115				120						125
Lys	Pro	Val	Val	Ile	Phe	Gly	Val	Phe	Ser	Val	Val	Ile	Phe	Asn	Ala
					130				135						140
Leu	Phe	Gly	Leu	Ser	Val	Thr	Tyr	Trp	Met	Ala	Ile	Ala	Thr	Arg	Phe
					145				150						160
Leu	Leu	Gly	Ala	Leu	Asn	Gly	Leu	Leu	Gly	Pro	Met	Lys	Ala	Tyr	Ala
					165				170						175
Ile	Glu	Val	Cys	Arg	Pro	Glu	His	Glu	Ala	Leu	Ala	Leu	Ser	Leu	Val
					180				185						190
Ser	Thr	Ala	Trp	Gly	Ile	Gly	Leu	Ile	Ile	Gly	Pro	Ala	Leu	Gly	Gly
					195				200						205
Tyr	Leu	Ala	Leu	Pro	Ala	Glu	Lys	Tyr	Pro	Asn	Ile	Phe	Ser	Pro	Asp
					210				215						220
Ser	Leu	Phe	Gly	Arg	Phe	Pro	Tyr	Phe	Leu	Pro	Cys	Leu	Cys	Thr	Ser
					225				230						240
Val	Phe	Ala	Ala	Ala	Val	Leu	Ile	Gly	Cys	Ile	Trp	Met	Pro	Glu	Thr
					245				250						255
Leu	His	Lys	His	Lys	Val	Asn	Glu	Asn	Arg	Asn	Gln	Ser	Val	Glu	Ser
					260				265						270

Leu Glu Ala His Leu Ile Asp Pro Lys Glu Lys Val Glu Gln Ser Asn
 275 280 285
 Ser Pro Asp Thr Lys Lys Ser Leu Phe Lys Asn Trp Pro Leu Met Ser
 290 295 300
 Ser Ile Ile Val Tyr Cys Val Phe Ser Phe His Asp Met Ala Tyr Thr
 305 310 315 320
 Glu Val Phe Ser Leu Trp Ala Glu Ser Asp Arg Thr Tyr Gly Gly Leu
 325 330 335
 Ser Leu Ser Ser Glu Asp Val Gly Gln Thr Leu Ala Ile Thr Gly Ser
 340 345 350
 Ser Leu Leu Val Tyr Gln Leu Phe Leu Tyr Pro Arg Ile Asn Arg Val
 355 360 365
 Leu Gly Pro Ile Lys Ser Ser Gln Ile Ala Ala Gly Ile Cys Ile Pro
 370 375 380
 Ile Leu Phe Ala Tyr Pro Tyr Met Thr Tyr Leu Ser Glu Pro Gly Leu
 385 390 395 400
 Ser Ile Val Leu Asn Ile Ala Ser Val Ile Lys Asn Asn Leu Gly Val
 405 410 415
 Thr Ile Ile Thr Gly Thr Phe Ile Leu Gln Asn Asn Ala Val Pro Gln
 420 425 430
 Asp Gln Arg Gly Ala Ala Asn Gly Leu Ala Met Thr Gly Met Ser Phe
 435 440 445
 Phe Lys Ala Val Ala Pro Ala Gly Ala Gly Ile Val Phe Ser Trp Ala
 450 455 460
 Gln Lys Arg Gln His Ala Phe Phe Pro Gly Asp Gln Met Val Phe
 465 470 475 480
 Phe Leu Leu Asn Ile Ile Glu Leu Leu Gly Leu Leu Leu Thr Phe Lys
 485 490 495
 Phe Phe Leu Ala Val Pro Asp Lys Ser Asp Ser Asn
 500 505

<210> 72
 <211> 522
 <212> PRT
 <213> Lolium perenne

<400> 72
 Met Ser Ser Met Gln Phe Ser Ser Val Leu Pro Leu Glu Gly Lys Ala
 1 5 10 15
 Cys Val Cys Pro Val Arg Ser Ala Asn Asn Gly Cys Glu Arg Leu Lys
 20 25 30
 Val Gly Asp Ser Ser Ser Leu Arg His Glu Met Ala Leu Arg Arg Lys
 35 40 45
 Cys Asn Gly Ala Arg Gly Gly Ala Ala Asn Gly Ala Gln Cys Val
 50 55 60
 Leu Thr Ser Asp Ala Ser Pro Asp Thr Leu Val Val Arg Ser Ser Phe
 65 70 75 80
 Arg Arg Asn Tyr Ala Asp Pro Asn Glu Val Ala Ala Val Ile Leu Gly
 85 90 95
 Gly Gly Thr Gly Thr Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr
 100 105 110
 Pro Ala Val Pro Ile Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met
 115 120 125
 Ser Asn Cys Phe Asn Ser Gly Ile Asn Lys Ile Phe Val Met Thr Gln
 130 135 140
 Phe Asn Ser Ala Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Gly
 145 150 155 160
 Gly Gly Ile Asn Phe Thr Asp Gly Ser Val Glu Val Leu Ala Ala Thr
 165 170 175
 Gln Met Pro Gly Glu Ala Ala Gly Trp Phe Arg Gly Thr Ala Asp Ala
 180 185 190
 Val Arg Lys Phe Ile Trp Val Leu Glu Asp Tyr Tyr Lys His Lys Ser
 195 200 205
 Ile Glu His Ile Leu Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asp
 210 215 220
 Tyr Met Glu Leu Val Gln Lys His Val Asp Asp Asn Ala Asp Ile Thr
 225 230 235 240
 Leu Ser Cys Ala Pro Val Gly Glu Ser Arg Ala Ser Glu Tyr Gly Leu

Val	Lys	Phe	Asp	245	Ser	Ser	Gly	Arg	Val	Ile	Gln	Phe	Ser	Glu	Lys	Pro
260					265							270				
Lys	Gly	Ala	Asp	Leu	Glu	Ala	Met	Lys	Val	Asp	Thr	Ser	Phe	Leu	Asn	
275					280							285				
Phe	Ala	Ile	Asp	Asp	Pro	Ala	Lys	Asn	Pro	Tyr	Ile	Ala	Ser	Met	Gly	
290					295						300					
Val	Tyr	Val	Phe	Lys	Arg	Glu	Val	Leu	Leu	Asn	Leu	Leu	Lys	Ser	Arg	
305					310					315				320		
Tyr	Thr	Glu	Leu	His	Asp	Phe	Gly	Ser	Glu	Ile	Leu	Pro	Arg	Ala	Leu	
325					330					335						
His	Asp	His	Asn	Val	Gln	Ala	Tyr	Val	Phe	Thr	Asp	Tyr	Trp	Glu	Asp	
340					345					350						
Ile	Gly	Thr	Ile	Arg	Ser	Phe	Phe	Asp	Ala	Asn	Met	Ala	Leu	Cys	Glu	
355					360					365						
Gln	Pro	Pro	Lys	Phe	Glu	Phe	Tyr	Asp	Pro	Lys	Thr	Pro	Phe	Phe	Thr	
370					375					380						
Ser	Pro	Arg	Tyr	Leu	Pro	Pro	Thr	Lys	Ser	Asp	Lys	Cys	Arg	Ile	Lys	
385					390					395				400		
Glu	Ala	Ile	Ile	Ser	His	Gly	Cys	Phe	Leu	Arg	Glu	Cys	Thr	Ile	Glu	
405					410					415						
His	Ser	Ile	Ile	Gly	Val	Arg	Ser	Arg	Leu	Asn	Ser	Gly	Ser	Val	Leu	
420					425					430						
Lys	Asn	Ala	Met	Met	Met	Gly	Ala	Asp	Leu	Tyr	Glu	Thr	Glu	Asp	Glu	
435					440					445						
Ile	Ser	Gly	Leu	Leu	Ser	Glu	Gly	Lys	Val	Pro	Ile	Gly	Val	Gly	Glu	
450					455					460						
Asn	Ser	Lys	Leu	Ser	Asn	Cys	Ile	Ile	Asp	Met	Asn	Ala	Arg	Ile	Gly	
465					470					475				480		
Arg	Asp	Asp	Val	Val	Ile	Ala	Asn	Ser	Glu	Gly	Val	Gln	Glu	Ala	Asp	Arg
485					490					495						
Pro	Glu	Glu	Gly	Tyr	Tyr	Ile	Arg	Ser	Gly	Ile	Val	Val	Ile	Leu	Lys	
500					505					510						
Asn	Ala	Thr	Val	Lys	Asp	Gly	Thr	Val	Val							
515					520											

<210> 73

<211> 522

<212> PRT

<213> Festuca arundinacea

<400> 73

Met	Ser	Ser	Met	Gln	Phe	Ser	Ser	Val	Leu	Pro	Leu	Glu	Gly	Lys	Ala	
1				5					10				15			
Cys	Val	Cys	Pro	Val	Arg	Ser	Ala	Asn	Asn	Gly	Cys	Glu	Arg	Leu	Lys	
								20	25				30			
Val	Gly	Asp	Ser	Ser	Ser	Leu	Arg	His	Glu	Met	Ala	Leu	Arg	Arg	Lys	
								35	40				45			
Cys	Asn	Gly	Ala	Arg	Gly	Gly	Ala	Ala	Asp	Gly	Ala	Gln	Cys	Val		
								50	55				60			
Leu	Thr	Ser	Asp	Ala	Ser	Pro	Asp	Thr	Leu	Val	Val	Arg	Ser	Ser	Phe	
								65	70				75			80
Arg	Met	Asn	Tyr	Ala	Asp	Pro	Asn	Glu	Val	Ala	Ala	Val	Ile	Leu	Gly	
								85	90				95			
Gly	Gly	Thr	Gly	Thr	Gly	Leu	Phe	Pro	Leu	Thr	Ser	Thr	Arg	Ala	Thr	
								100	105				110			
Pro	Ala	Val	Pro	Ile	Gly	Gly	Cys	Tyr	Arg	Leu	Ile	Asp	Ile	Pro	Met	
								115	120				125			
Ser	Asn	Cys	Phe	Asn	Ser	Gly	Ile	Asn	Lys	Ile	Phe	Val	Met	Thr	Gln	
								130	135				140			
Phe	Asn	Ser	Ala	Ser	Leu	Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Gly	
								145	150				155			160
Gly	Gly	Ile	Asn	Phe	Thr	Asp	Gly	Ser	Val	Glu	Val	Leu	Ala	Ala	Thr	
								165	170				175			
Gln	Met	Pro	Gly	Glu	Ala	Ala	Gly	Trp	Phe	Arg	Gly	Thr	Ala	Asp	Ala	
								180	185				190			
Val	Arg	Lys	Phe	Ile	Trp	Val	Leu	Glu	Asp	Tyr	Tyr	Lys	His	Lys	Ser	
								195	200				205			

Ile Glu His Ile Leu Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asp
 210 215 220
 Tyr Met Glu Leu Val Gln Lys His Val Asp Asp Asn Ala Asp Ile Thr
 225 230 235 240
 Leu Ser Cys Ala Pro Val Gly Glu Ser Arg Ala Ser Glu Tyr Gly Leu
 245 250 255
 Val Lys Phe Asp Ser Ser Gly Arg Val Ile Gln Phe Ser Glu Lys Pro
 260 265 270
 Lys Gly Ala Asp Leu Glu Ala Met Lys Val Asp Thr Ser Phe Leu Asn
 275 280 285
 Phe Ala Ile Asp Asp Pro Ala Lys Asn Pro Tyr Ile Ala Ser Met Gly
 290 295 300
 Val Tyr Val Phe Lys Arg Glu Val Leu Leu Asn Leu Leu Lys Ser Arg
 305 310 315 320
 Tyr Thr Glu Leu His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Leu
 325 330 335
 His Asp His Asn Val Gln Ala Tyr Val Phe Thr Asp Tyr Trp Glu Asp
 340 345 350
 Ile Gly Thr Ile Arg Ser Phe Phe Asp Ala Asn Met Ala Leu Cys Glu
 355 360 365
 Gln Pro Pro Lys Phe Glu Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr
 370 375 380
 Ser Pro Arg Tyr Leu Pro Pro Thr Lys Ser Asp Lys Cys Arg Ile Lys
 385 390 395 400
 Glu Ala Ile Ile Ser His Gly Cys Phe Leu Arg Glu Cys Thr Ile Glu
 405 410 415
 His Ser Ile Ile Gly Val Arg Ser Arg Leu Asn Ser Gly Ser Val Leu
 420 425 430
 Lys Asn Ala Met Met Met Gly Ala Asp Leu Tyr Glu Thr Glu Asp Glu
 435 440 445
 Ile Ser Gly Leu Leu Ser Glu Gly Lys Val Pro Ile Gly Val Gly Glu
 450 455 460
 Asn Ser Lys Leu Ser Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly
 465 470 475 480
 Arg Asp Val Val Ile Ala Asn Ser Glu Gly Val Gln Glu Ala Asp Arg
 485 490 495
 Pro Glu Glu Gly Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys
 500 505 510
 Asn Ala Thr Val Lys Asp Gly Thr Val Val
 515 520

<210> 74
<211> 525
<212> PRT
<213> Lolium perenne

<400> 74
 Met Thr Gly Ala Pro Pro Ser Thr Val Met Ala Met Gly Ala Ala Thr
 1 5 10 15
 Ser Pro Cys Lys Ile Leu Ser Ala Thr Gln Arg Ala Ser Thr Ala Ala
 20 25 30
 Ala Ser Ala Ser Thr Ser Arg Glu Ser Val Ser Leu Arg Ala Pro Arg
 35 40 45
 Gly Arg Arg Gln Arg Pro Arg Pro Arg Gly Leu Ala Leu Ser Leu Ala
 50 55 60
 Pro Ala Arg Arg Pro Phe Val Phe Ser Pro Arg Ala Val Ser Asp Ser
 65 70 75 80
 Lys Ser Ser Gln Thr Cys Leu Asp Pro Asp Ala Ser Thr Ser Val Leu
 85 90 95
 Gly Ile Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr
 100 105 110
 Lys Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu
 115 120 125
 Ile Asp Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile
 130 135 140
 Tyr Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser
 145 150 155 160
 Arg Ala Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val

Glu	Val	Leu	Ala	Ala	Gln	Gln	Ser	Pro	Asp	Asn	Pro	Asn	Trp	Phe	Gln
165															
180															
Gly	Thr	Ala	Asp	Ala	Val	Arg	Gln	Tyr	Leu	Trp	Leu	Phe	Glu	Glu	His
185															
195															
Asn	Val	Met	Glu	Tyr	Leu	Ile	Leu	Ala	Gly	Asp	His	Leu	Tyr	Arg	Met
200															
210															
Asp	Tyr	Glu	Lys	Phe	Ile	Gln	Ala	His	Arg	Glu	Thr	Asp	Ala	Asp	Ile
225															
230															
Thr	Val	Ala	Ala	Leu	Pro	Met	Asp	Glu	Glu	Arg	Ala	Thr	Ala	Phe	Gly
245															
250															
Leu	Met	Lys	Ile	Asp	Glu	Glu	Gly	Arg	Ile	Val	Glu	Phe	Ala	Glu	Lys
260															
265															
Pro	Lys	Gly	Glu	Gln	Leu	Lys	Ala	Met	Met	Val	Asp	Thr	Thr	Ile	Leu
275															
280															
Gly	Leu	Asp	Asp	Val	Arg	Ala	Lys	Glu	Met	Pro	Tyr	Ile	Ala	Ser	Met
290															
295															
Gly	Ile	Tyr	Val	Ile	Ser	Lys	His	Val	Met	Leu	Gln	Leu	Leu	Arg	Asp
305															
310															
Gln	Phe	Pro	Gly	Ala	Asn	Asp	Phe	Gly	Ser	Glu	Val	Ile	Pro	Gly	Ala
325															
330															
Thr	Ser	Thr	Gly	Met	Arg	Val	Gln	Ala	Tyr	Leu	Tyr	Asp	Gly	Tyr	Trp
340															
345															
Glu	Asp	Ile	Gly	Thr	Ile	Glu	Ala	Phe	Tyr	Asn	Ala	Asn	Leu	Gly	Ile
355															
360															
Thr	Lys	Pro	Ile	Pro	Asp	Phe	Ser	Phe	Tyr	Asp	Arg	Ser	Ala	Pro	
370															
375															
Ile	Tyr	Thr	Gln	Pro	Arg	His	Leu	Pro	Pro	Ser	Lys	Val	Leu	Asp	Ala
385															
390															
Asp	Val	Thr	Asp	Ser	Val	Ile	Gly	Glu	Gly	Cys	Val	Ile	Lys	Asn	Cys
405															
410															
Lys	Ile	His	His	Ser	Val	Val	Gly	Leu	Arg	Ser	Cys	Ile	Ser	Glu	Gly
420															
425															
Ala	Ile	Ile	Glu	Asp	Thr	Leu	Leu	Met	Gly	Ala	Asp	Tyr	Tyr	Glu	Thr
435															
440															
Glu	Ala	Asp	Lys	Lys	Leu	Leu	Ala	Asp	Lys	Gly	Gly	Ile	Pro	Ile	Gly
450															
455															
Ile	Gly	Lys	Asn	Ser	His	Ile	Arg	Arg	Ala	Ile	Ile	Asp	Lys	Asn	Ala
465															
470															
Arg	Ile	Gly	Asp	Asn	Val	Lys	Ile	Ile	Asn	Val	Asp	Asn	Val	Gln	Glu
485															
490															
Ala	Ala	Arg	Glu	Thr	Asp	Gly	Tyr	Phe	Ile	Lys	Ser	Gly	Ile	Val	Thr
500															
505															
val	Ile	Lys	Asp	Ala	Leu	Leu	Pro	Ser	Gly	Thr	Val	Ile			
515															

<210> 75

<211> 524

<212> PRT

<213> Festuca arundinacea

<400> 75

Met	Thr	Arg	Ala	Pro	Pro	Ser	Thr	Val	Met	Ala	Met	Gly	Ala	Ala	Thr
1															
Ser	Pro	Cys	Lys	Ile	Leu	Ser	Ala	Thr	Gln	Arg	Ala	Ser	Ala	Ala	Ala
20															
Pro	Ser	Ala	Ser	Thr	Ser	Arg	Glu	Ser	Val	Cys	Leu	Leu	Arg	Ala	Pro
35															
Arg	Gly	Arg	Arg	Gln	Arg	Pro	Arg	Gly	Leu	Ala	Leu	Ser	Leu	Ala	Pro
50															
Ala	Arg	Arg	Pro	Phe	Val	Phe	Ser	Pro	Arg	Ala	Val	Ser	Asp	Ser	Lys
65															
Ser	Ser	Gln	Thr	Cys	Leu	Asp	Pro	Asp	Ala	Ser	Thr	Ser	Val	Leu	Gly
85															
Ile	Ile	Leu	Gly	Gly	Gly	Ala	Gly	Thr	Arg	Leu	Tyr	Pro	Leu	Thr	Lys
100															
Lys	Arg	Ala	Lys	Pro	Ala	Val	Pro	Leu	Gly	Ala	Asn	Tyr	Arg	Leu	Ile
115															

Asp Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr
 130 135 140
 Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg
 145 150 155 160
 Ala Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu
 165 170 175
 Val Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly
 180 185 190
 Thr Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn
 195 200 205
 Val Met Glu Tyr Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp
 210 215 220
 Tyr Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asp Ala Asp Ile Thr
 225 230 235 240
 Val Ala Ala Leu Pro Met Asp Glu Glu Arg Ala Thr Ala Phe Gly Leu
 245 250 255
 Met Lys Ile Asp Glu Glu Gly Arg Ile Val Glu Phe Ala Glu Lys Pro
 260 265 270
 Lys Gly Glu Gln Leu Lys Ala Met Val Asp Thr Thr Ile Leu Gly
 275 280 285
 Leu Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly
 290 295 300
 Ile Tyr Val Ile Ser Lys His Val Met Leu Gln Leu Leu Arg Asp Gln
 305 310 315 320
 Phe Pro Gly Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr
 325 330 335
 Ser Thr Gly Met Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu
 340 345 350
 Asp Ile Gly Thr Ile Glu Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr
 355 360 365
 Lys Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Ser Ala Pro Ile
 370 375 380
 Tyr Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp
 385 390 395 400
 Val Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys
 405 410 415
 Ile His His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala
 420 425 430
 Ile Ile Glu Asp Thr Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu
 435 440 445
 Ala Asp Lys Lys Leu Leu Ala Asp Lys Gly Gly Ile Pro Ile Gly Ile
 450 455 460
 Gly Lys Asn Ser His Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg
 465 470 475 480
 Ile Gly Asp Asn Val Lys Ile Ile Asn Val Asp Asn Val Gln Glu Ala
 485 490 495
 Ala Arg Glu Thr Asp Gly Tyr Phe Ile Lys Ser Gly Ile Val Thr Val
 500 505 510
 Ile Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile
 515 520

<210> 76

<211> 398

<212> PRT

<213> Festuca arundinacea

<400> 76

Met Ala Ala Thr Met Thr Val Glu Glu Val Arg Lys Ala Gln Arg Ala
 1 5 10 15
 Glu Gly Pro Ala Thr Val Leu Ala Ile Gly Thr Ala Thr Pro Ala Asn
 20 25 30
 Cys Val Tyr Gln Ala Asp Tyr Pro Asp Tyr Tyr Phe Lys Ile Thr Lys
 35 40 45
 Ser Asp His Leu Ala Asp Leu Lys Glu Lys Phe Lys Arg Met Cys Asp
 50 55 60
 Lys Ser Gln Ile Arg Lys Arg Tyr Met His Leu Thr Glu Glu Ile Leu
 65 70 75 80
 Glu Glu Asn Pro Asn Met Cys Ala Tyr Met Ala Pro Ser Leu Asp Ala

85 90 95

Arg Gln Asp Ile Val Val Val Glu Val Pro Lys Leu Gly Lys Ala Ala
 100 105 110
 Ala Gln Lys Ala Ile Lys Glu Trp Gly Gln Pro Arg Ser Lys Ile Thr
 115 120 125
 His Leu Val Phe Cys Thr Thr Ser Gly Val Asp Met Pro Gly Ala Asp
 130 135 140
 Tyr Gln Leu Thr Lys Met Leu Gly Leu Arg Pro Ser Val Lys Arg Leu
 145 150 155 160
 Met Met Tyr Gln Gln Gly Cys Phe Ala Gly Gly Thr Val Leu Arg Leu
 165 170 175
 Ala Lys Asp Leu Ala Glu Asn Asn Arg Gly Ala Arg Val Leu Val Val
 180 185 190
 Cys Ser Glu Ile Thr Ala Val Thr Phe Arg Gly Pro His Glu Ser His
 195 200 205
 Leu Asp Ser Leu Val Gly Gln Ala Leu Phe Gly Asp Gly Ala Ala Ala
 210 215 220
 Val Ile Ile Gly Ala Asp Pro Asp Val Ser Val Glu Arg Pro Leu Phe
 225 230 235 240
 Gln Leu Val Ser Val Ser Gln Thr Ile Leu Pro Asp Ser Glu Gly Ala
 245 250 255
 Ile Asp Gly His Leu Arg Glu Val Gly Leu Thr Phe His Leu Leu Lys
 260 265 270
 Asp Val Pro Gly Leu Ile Ser Lys Asn Ile Glu Arg Ala Leu Glu Glu
 275 280 285
 Ala Phe Lys Pro Leu Gly Ile Asp Asp Trp Asn Ser Val Phe Trp Val
 290 295 300
 Ala His Pro Gly Gly Pro Ala Ile Leu Asp Met Val Glu Ala Lys Val
 305 310 315 320
 Asn Leu Asn Lys Glu Arg Met Arg Ala Thr Arg His Val Leu Ser Glu
 325 330 335
 Tyr Gly Asn Met Ser Ser Ala Cys Val Leu Phe Ile Met Asp Glu Met
 340 345 350
 Arg Lys Arg Ser Ala Glu Asp Gly His Thr Thr Thr Gly Glu Gly Met
 355 360 365
 Asp Trp Gly Val Leu Phe Gly Phe Gly Pro Gly Leu Thr Val Glu Thr
 370 375 380
 Val Val Leu His Ser Met Pro Ile Ala Ala Asp Ala Thr Ala
 385 390 395

<210> 77

<211> 398

<212> PRT

<213> Festuca arundinacea

<400> 77

Met Ala Thr Thr Met Thr Val Glu Glu Val Arg Lys Ala Gln Arg Ala
 1 5 10 15
 Glu Gly Pro Ala Thr Val Leu Ala Ile Gly Thr Ala Thr Pro Ala Asn
 20 25 30
 Cys Val Tyr Gln Ala Asp Tyr Pro Asp Tyr Tyr Phe Lys Ile Thr Lys
 35 40 45
 Ser Asp His Leu Ala Asp Leu Lys Glu Lys Phe Lys Arg Met Cys Asp
 50 55 60
 Lys Ser Gln Ile Arg Lys Arg Tyr Met His Leu Thr Glu Glu Ile Leu
 65 70 75 80
 Glu Glu Asn Pro Asn Met Cys Ala Tyr Met Ala Pro Ser Leu Asp Ala
 85 90 95
 Arg Gln Asp Ile Val Val Val Glu Val Pro Lys Leu Gly Lys Ala Ala
 100 105 110
 Ala Gln Lys Ala Ile Lys Glu Trp Gly Gln Pro Arg Ser Lys Ile Thr
 115 120 125
 His Leu Val Phe Cys Thr Thr Ser Gly Val Asp Met Pro Gly Ala Asp
 130 135 140
 Tyr Gln Leu Thr Lys Met Leu Gly Leu Arg Pro Ser Val Lys Arg Leu
 145 150 155 160
 Met Met Tyr Gln Gln Gly Cys Phe Ala Gly Gly Thr Val Leu Arg Leu
 165 170 175

Ala Lys Asp Leu Ala Glu Asn Asn Arg Gly Ala Arg Val Leu Val Val
 180 185 190
 Cys Ser Glu Ile Thr Ala Val Thr Phe Arg Gly Pro His Glu Ser His
 195 200 205
 Leu Asp Ser Leu Val Gly Gln Ala Leu Phe Gly Asp Gly Ala Ala Ala
 210 215 220
 Val Ile Ile Gly Ala Asp Pro Asp Val Ser Val Glu His Pro Leu Phe
 225 230 235 240
 Gln Leu Val Ser Ala Ser Gln Thr Ile Leu Pro Asp Ser Glu Gly Ala
 245 250 255
 Ile Asp Gly His Leu Arg Glu Val Gly Leu Thr Phe His Leu Leu Lys
 260 265 270
 Asp Val Pro Gly Leu Ile Ser Lys Asn Ile Glu Arg Ala Leu Glu Glu
 275 280 285
 Ala Phe Lys Pro Leu Gly Ile Asp Asp Trp Asn Ser Val Phe Trp Val
 290 295 300
 Ala His Pro Gly Gly Pro Ala Ile Leu Asp Met Val Glu Ala Lys Val
 305 310 315 320
 Asn Leu Asn Lys Glu Arg Met Arg Ala Thr Arg His Val Leu Ser Glu
 325 330 335
 Tyr Gly Asn Met Ser Ser Ala Cys Val Leu Phe Ile Met Asp Glu Met
 340 345 350
 Arg Lys Arg Ser Ala Glu Asp Gly His Thr Thr Thr Gly Glu Gly Met
 355 360 365
 Asp Trp Gly Val Leu Phe Gly Phe Gly Pro Gly Leu Thr Val Glu Thr
 370 375 380
 Val Val Leu His Ser Met Pro Ile Ala Ala Gly Ala Thr Ala
 385 390 395

<210> 78

<211> 277

<212> PRT

<213> Festuca arundinacea

<400> 78

Arg Ala Asp Leu Glu Glu Gly Ser Phe Asp Asp Ala Val Ala Gly
 1 5 10 15
 Cys Asp Tyr Ala Phe Leu Val Ala Ala Pro Val Asn Leu Lys Ala Glu
 20 25 30
 Asn Pro Glu Lys Asp Met Val Glu Pro Ala Val Gly Gly Thr Leu Asn
 35 40 45
 Ala Met Arg Ser Cys Val Arg Ala Gly Thr Val Lys Arg Val Val Leu
 50 55 60
 Thr Ser Ser Val Ala Ser Val Ser Ala Arg Pro Leu Leu Gln Gly Asp
 65 70 75 80
 Gly His Val Leu Asp Glu Glu Ser Trp Ser Asp Val Asp Phe Leu Arg
 85 90 95
 Ala Lys Ala Thr Gly His Trp Gly Tyr Pro Val Ser Lys Val Leu Leu
 100 105 110
 Glu Lys Ala Ala Cys Ala Phe Ala Gln Ala Ser Gly Ile Ser Leu Val
 115 120 125
 Thr Val Cys Pro Val Val Val Gly Lys Ala Pro Ala Val Gln Val
 130 135 140
 His Thr Ser Val Pro Asp Val Leu Ser Pro Leu Ser Gly Asp Glu Ala
 145 150 155 160
 Lys Ile Gln Ile Leu Gln His Ile Glu Arg Ala Ser Gly Ser Ile Ser
 165 170 175
 Leu Val His Val Asp Asp Leu Cys Arg Ala Glu Val Phe Leu Ala Glu
 180 185 190
 Glu Glu Ala Val Ala Ser Gly Arg Tyr Ile Cys Cys Ser Leu Ser Thr
 195 200 205
 Thr Ala Gly Val Leu Ala Arg Phe Leu Ser Val Lys Tyr Pro Gln Tyr
 210 215 220
 Lys Val Arg Thr Asp Arg Phe Ser Gly Ser Pro Glu Lys Pro Arg Val
 225 230 235 240
 Cys Met Ser Ser Ala Lys Leu Val Ala Glu Gly Phe Gln Tyr Lys Tyr
 245 250 255
 Lys Thr Leu Asp Glu Ile Tyr Asp Asp Val Val Glu Tyr Gly Arg Ala

Leu Gly Ile 260
275

265

270

<210> 79
<211> 342
<212> PRT
<213> Festuca arundinacea

<400> 79
Met Ala Ala Ala Gly Asp Gly Ser Arg Arg Lys Thr Ala Cys Val Thr
1 5 10 15
Gly Gly Asn Gly Tyr Ile Ala Ser Ala Leu Val Lys Met Leu Leu Glu
20 25 30
Lys Gly Tyr Ala Val Lys Thr Thr Val Arg Asn Pro Asp Asp Met Glu
35 40 45
Lys Asn Ser His Leu Lys Asp Leu Gln Ala Leu Gly Pro Leu Glu Val
50 55 60
Phe Arg Ala Asp Leu Gln Glu Glu Gly Ser Phe Asp Asp Ala Val Ala
65 70 75 80
Gly Cys Asp Tyr Ala Phe Leu Val Ala Ala Pro Val Asn Leu Lys Ala
85 90 95
Glu Asn Pro Glu Asp Met Val Glu Pro Ala Val Gly Thr Leu
100 105 110
Asn Ala Met Arg Ser Cys Val Arg Ala Gly Thr Val Lys Arg Val Val
115 120 125
Leu Thr Ser Ser Val Ala Ser Val Ser Ala Arg Pro Leu Leu Gln Gly
130 135 140
Asp Gly His Val Leu Asp Glu Glu Ser Trp Ser Asp Val Asp Phe Leu
145 150 155 160
Arg Ala Lys Ala Thr Gly His Trp Gly Tyr Pro Val Ser Lys Val Leu
165 170 175
Leu Glu Lys Ala Ala Cys Ala Phe Ala Gln Ala Ser Gly Ile Ser Leu
180 185 190
Val Thr Val Cys Pro Val Val Val Gly Lys Ala Pro Ala Val Gln
195 200 205
Val His Thr Ser Val Pro Asp Val Leu Ser Pro Leu Ser Gly Asp Glu
210 215 220
Ala Lys Ile Gln Ile Leu Gln His Ile Glu Arg Ala Ser Gly Ser Ile
225 230 235 240
Ser Leu Val His Val Asp Asp Leu Cys Arg Ala Glu Val Phe Leu Ala
245 250 255
Glu Glu Glu Ala Val Ala Ser Gly Arg Tyr Ile Cys Cys Ser Leu Ser
260 265 270
Thr Thr Ala Gly Val Leu Ala Arg Phe Leu Ser Val Lys Tyr Pro Gln
275 280 285
Tyr Lys Val Arg Thr Asp Arg Phe Ser Gly Ser Pro Glu Lys Pro Arg
290 295 300
Val Cys Met Ser Ser Ala Lys Leu Val Ala Glu Gly Phe Gln Tyr Lys
305 310 315 320
Tyr Lys Thr Leu Asp Glu Ile Tyr Asp Asp Val Val Glu Tyr Gly Arg
325 330 335
Ala Leu Gly Ile Leu Pro
340

<210> 80
<211> 255
<212> PRT
<213> Lolium perenne

<400> 80
Phe Ile Ser Val Thr Val Phe Tyr Val Val Gly Leu Arg Gln Arg Asp
1 5 10 15
Leu Val Gln Ala Gly Val Gln Gly Thr Leu Asn Val Met Arg Ser Cys
20 25 30
Val Lys Ala Gly Thr Val Lys Arg Val Ile Leu Thr Ser Ser Asp Ser
35 40 45
Ala Val Cys Gln Arg Pro Leu Glu Gly Asp Gly His Val Leu Asp Glu

Gly	Ser	Trp	Ser	Asp	Val	Pro	Tyr	Leu	Arg	Ala	Gln	Pro	Glu	Ala
65					70			75						80
Trp	Gly	Tyr	Ala	Val	Ser	Lys	Val	Leu	Met	Glu	Glu	Ala	Ala	Gly
														Lys
					85			90						95
Phe	Ala	Asp	Glu	Asn	Gly	Leu	Gly	Leu	Val	Ser	Val	Leu	Pro	Thr
														Phe
					100			105						110
Thr	Leu	Gly	Ala	Ala	Pro	Val	Ser	Gln	Ala	Arg	Thr	Ser	Val	Pro
														Val
115					120									125
Val	Leu	Ser	Leu	Leu	Ser	Gly	Asp	Glu	Glu	Gln	Leu	Asn	Leu	Glu
130					135									140
Ala	Met	His	Leu	Ile	Thr	Glu	Ser	Val	Ser	Ile	Asn	His	Ile	Asp
														Asp
145					150									160
Leu	Cys	Arg	Ala	Gln	Val	Phe	Leu	Ala	Glu	Asn	Glu	Ala	Ser	Gly
165								170						175
Arg	Tyr	Ile	Cys	Ser	Ser	His	Asp	Thr	Thr	Val	Val	Gln	Leu	Ala
														Arg
180								185						190
Leu	Leu	Ala	Asp	Lys	Tyr	Pro	Gln	Tyr	Asn	Val	Lys	Ser	Gln	Arg
														Phe
195					200									205
Asp	Gly	Ser	Pro	Glu	Lys	Pro	Arg	Val	Cys	Leu	Ser	Ser	Gln	Lys
														Leu
210								215						220
Ile	Gly	Glu	Gly	Phe	Val	Tyr	Lys	Tyr	Asp	Asp	Leu	Gly	Ala	Ile
														Leu
225					230					235				240
Asp	Asp	Leu	Val	Glu	Tyr	Gly	Arg	Thr	Thr	Gly	Ile	Leu	Pro	Phe
245									250					255

<210> 81

<211> 340

<212> PRT

<213> Lolium perenne

<400>	81													
Met	Ala	Ser	Ala	Ala	Gly	Gly	Arg	Arg	Lys	Thr	Ala	Cys	Val	Thr
1					5				10					15
Gly	Ser	Gly	Tyr	Ile	Ala	Ser	Ala	Leu	Ile	Lys	Thr	Leu	Leu	Asp
									25					30
					20									
Gly	Tyr	Ala	Val	Lys	Thr	Thr	Val	Arg	Asn	Pro	Asp	Asp	Leu	Glu
														Lys
35								40						45
Thr	Ser	His	Leu	Lys	Asp	Leu	Gln	Ala	Phe	Gly	Pro	Leu	Glu	Ile
														Phe
50								55						60
Arg	Gly	Glu	Leu	Asp	Val	Glu	Gly	Ser	Phe	Asp	Asp	Ser	Val	Ser
														Gly
65					70				75					80
Cys	Asp	Tyr	Val	Phe	Leu	Val	Ala	Ala	Pro	Met	Asp	Met	Gly	Ser
														Leu
85								90						95
Asn	Pro	Glu	Arg	Asp	Leu	Val	Gln	Ala	Gly	Val	Gln	Gly	Thr	Leu
														Asn
100								105						110
Val	Met	Arg	Ser	Cys	Val	Lys	Ala	Gly	Thr	Val	Lys	Arg	Val	Ile
														Leu
115								120						125
Thr	Ser	Ser	Asp	Ser	Ala	Val	Cys	Gln	Arg	Pro	Leu	Glu	Gly	Asp
														Gly
130								135						140
His	Val	Leu	Asp	Glu	Gly	Ser	Trp	Ser	Asp	Val	Pro	Tyr	Leu	Arg
														Ala
145					150				155					160
Glu	Gln	Pro	Glu	Ala	Trp	Gly	Tyr	Ala	Val	Ser	Lys	Val	Leu	Met
														Glu
165								170						175
Glu	Ala	Ala	Gly	Lys	Phe	Ala	Asp	Glu	Asn	Gly	Leu	Gly	Leu	Val
														Ser
180								185						190
Val	Leu	Pro	Thr	Phe	Thr	Leu	Gly	Ala	Ala	Pro	Val	Ser	Gln	Ala
														Arg
195								200						205
Thr	Ser	Val	Pro	Val	Val	Leu	Ser	Leu	Leu	Ser	Gly	Asp	Glu	Gln
210								215						220
Leu	Asn	Leu	Leu	Glu	Ala	Met	His	Leu	Ile	Thr	Glu	Ser	Val	Ile
														Leu
225					230					235				240
Asn	His	Ile	Asp	Asp	Leu	Cys	Arg	Ala	Gln	Val	Phe	Leu	Ala	Glu
														Asn
245								250						255
Glu	Ala	Ser	Ser	Gly	Arg	Tyr	Ile	Cys	Ser	Ser	His	Asp	Thr	Thr
														Val
260								265						270
Val	Gln	Leu	Ala	Arg	Leu	Leu	Ala	Asp	Lys	Tyr	Pro	Gln	Tyr	Asn
														Val
275								280						285

Lys Ser Gln Arg Phe Asp Gly Ser Pro Glu Lys Pro Arg Val Cys Leu
 290 295 300
 Ser Ser Gln Lys Leu Ile Gly Glu Gly Phe Val Tyr Lys Tyr Asp Asp
 305 310 315 320
 Leu Gly Ala Ile Leu Asp Asp Leu Val Glu Tyr Gly Arg Thr Thr Gly
 325 330 335
 Ile Leu Pro Phe
 340

<210> 82
 <211> 508
 <212> PRT
 <213> Lolium perenne

<400> 82
 Ala Ala Ala Ser Ile Trp Phe Leu Phe Arg Gly Ser Ser Ser Gly Lys
 1 5 10 15
 Lys Leu Ser Lys Leu Pro Leu Pro Pro Gly Pro Arg Gly Trp Pro Val
 20 25 30
 Leu Gly Asn Leu Pro Gln Val Gly Ala Lys Pro His His Thr Met Ala
 35 40 45
 Ala Leu Ser Gln Gln Phe Gly Pro Leu Phe Arg Leu Arg Phe Gly Val
 50 55 60
 Ala Glu Val Val Val Ala Ala Ser Ala Lys Val Ala Ser Gln Phe Leu
 65 70 75 80
 Arg Ala His Asp Ala Asn Phe Ser Asp Arg Pro Pro Asn Ser Gly Ala
 85 90 95
 Glu His Val Ala Tyr Asn Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly
 100 105 110
 Ser Arg Trp Arg Ala Leu Arg Lys Leu Cys Ala Leu His Leu Phe Ser
 115 120 125
 Ala Lys Ala Leu Asp Ala Leu Arg Ala Val Arg Glu Ala Glu Val Ala
 130 135 140
 Leu Met Val Lys Gln Leu Lys Glu Ser Ala Pro Ala Gly Val Val Val
 145 150 155 160
 Gly Gln Glu Ala Asn Val Cys Ala Thr Asn Ala Leu Ala Arg Ala Ala
 165 170 175
 Val Gly Arg Arg Val Phe Gly Gly Ser Ala Gly Glu Gly Ala Arg Glu
 180 185 190
 Phe Lys Asp Met Val Val Glu Leu Met Gln Leu Ala Gly Val Phe Asn
 195 200 205
 Ile Gly Asp Phe Val Pro Ala Leu Arg Trp Leu Asp Pro Gln Gly Val
 210 215 220
 Val Ala Arg Met Lys Arg Leu His Arg Arg Tyr Asp Ala Met Met Asp
 225 230 235 240
 Gly Phe Ile Ser Gln Arg Asp Gln Arg His Asn Gln Ala Ala Ala Asp
 245 250 255
 Gly Glu Arg Lys Asp Leu Leu Ser Val Met Leu Gly Tyr Met Arg Pro
 260 265 270
 Asp Gly Gly Gly Glu Glu Glu Gly Ile Ser Phe Asn His Thr Asp
 275 280 285
 Ile Lys Ala Leu Leu Leu Asn Leu Phe Thr Ala Gly Thr Asp Thr Thr
 290 295 300
 Ser Ser Thr Val Glu Trp Ala Leu Ala Glu Leu Ile Arg His Lys Asp
 305 310 315 320
 Val Leu Thr Gln Ala Gln Arg Glu Leu Asp Asp Ile Val Gly Gln Asp
 325 330 335
 Arg Leu Val Thr Glu Ser Asp Leu Pro His Leu Thr Phe Leu Thr Ala
 340 345 350
 Val Ile Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro Leu Ser Leu
 355 360 365
 Pro Arg Val Ala Thr Glu Asp Cys Glu Val Glu Gly Tyr Arg Ile Pro
 370 375 380
 Lys Gly Thr Thr Leu Leu Val Asn Val Trp Ala Ile Ala Arg Asp Pro
 385 390 395 400
 Ala Ser Trp Gly Pro Asp Ala Leu Glu Phe Arg Pro Ala Arg Phe Leu
 405 410 415
 Ala Gly Gly Leu His Glu Ser Val Asp Val Lys Gly Ser Asp Tyr Glu

Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Leu Ser Trp
 420 425 430
 435 440 445
 Gly Leu Arg Met Val Thr Leu Met Thr Ala Thr Leu Val His Ala Phe
 450 455 460
 Asp Trp Ser Leu Val Asp Gly Leu Thr Pro Glu Lys Leu Asp Met Glu
 465 470 475 480
 Glu Ala Tyr Gly Leu Thr Leu Gln Arg Ala Ala Pro Leu Met Val Arg
 485 490 495
 Pro Ile Pro Arg Leu Leu Ser Ser Ala Tyr Thr Val
 500 505

<210> 83

<211> 524

<212> PRT

<213> Lolium perenne

<400> 83

Met Asp His Arg Asp Val Leu Val Leu Leu Cys Ser Leu Ala Ala Leu
 1 5 10 15
 Ala Ala Ala Ser Ile Trp Phe Leu Phe Arg Gly Ser Ser Ser Gly Lys
 20 25 30
 Lys Leu Ser Lys Leu Pro Leu Pro Pro Gly Pro Arg Gly Trp Pro Val
 35 40 45
 Leu Gly Asn Leu Pro Gln Val Gly Ala Lys Pro His His Thr Met Ala
 50 55 60
 Ala Leu Ser Gln Gln Phe Gly Pro Leu Phe Arg Leu Arg Phe Gly Val
 65 70 75 80
 Ala Glu Val Val Val Ala Ala Ser Ala Lys Val Ala Ser Gln Phe Leu
 85 90 95
 Arg Ala His Asp Ala Asn Phe Ser Asp Arg Pro Pro Asn Ser Gly Ala
 100 105 110
 Glu His Val Ala Tyr Asn Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly
 115 120 125
 Ser Arg Trp Arg Ala Leu Arg Lys Leu Cys Ala Leu His Leu Phe Ser
 130 135 140
 Ala Lys Ala Leu Asp Ala Leu Arg Ala Val Arg Glu Ala Glu Val Ala
 145 150 155 160
 Leu Met Val Lys Gln Leu Lys Glu Ser Ala Pro Ala Gly Val Val Val
 165 170 175
 Gly Gln Glu Ala Asn Val Cys Ala Thr Asn Ala Leu Ala Arg Ala Ala
 180 185 190
 Val Gly Arg Arg Val Phe Gly Gly Ser Ala Gly Glu Gly Ala Arg Glu
 195 200 205
 Phe Lys Asp Met Val Val Glu Leu Met Gln Leu Ala Gly Val Phe Asn
 210 215 220
 Ile Gly Asp Phe Val Pro Ala Leu Arg Trp Leu Asp Pro Gln Gly Val
 225 230 235 240
 Val Ala Arg Met Lys Arg Leu His Arg Arg Tyr Asp Ala Met Met Asp
 245 250 255
 Gly Phe Ile Ser Glu Arg Asp Gln Arg His Asn Gln Ala Ala Asp
 260 265 270
 Gly Glu Arg Lys Asp Leu Leu Ser Val Met Leu Gly Tyr Met Arg Pro
 275 280 285
 Asp Gly Gly Gly Glu Glu Gly Ile Ser Phe Asn His Thr Asp
 290 295 300
 Ile Lys Ala Leu Leu Leu Asn Leu Phe Thr Ala Gly Thr Asp Thr Thr
 305 310 315 320
 Ser Ser Thr Val Glu Trp Ala Leu Ala Glu Leu Ile Arg His Lys Asp
 325 330 335
 Val Leu Thr Gln Ala Gln Arg Glu Leu Asp Asp Ile Val Gly Gln Asp
 340 345 350
 Arg Leu Val Thr Glu Ser Asp Leu Pro His Leu Thr Phe Leu Thr Ala
 355 360 365
 Val Ile Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro Leu Ser Leu
 370 375 380
 Pro Arg Val Ala Thr Glu Asp Cys Glu Val Glu Gly Tyr Arg Ile Pro
 385 390 395 400

Lys Gly Thr Thr Leu Leu Val Asn Val Trp Ala Ile Ala Arg Asp Pro
 405 410 415
 Ala Ser Trp Gly Pro Asp Ala Leu Glu Phe Arg Pro Ala Arg Phe Leu
 420 425 430
 Ala Gly Gly Leu His Glu Ser Val Asp Val Lys Gly Ser Asp Tyr Glu
 435 440 445
 Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Leu Ser Trp
 450 455 460
 Gly Leu Arg Met Val Thr Leu Met Thr Ala Thr Leu Val His Ala Phe
 465 470 475 480
 Asp Trp Ser Leu Val Asp Gly Leu Thr Pro Glu Lys Leu Asp Met Glu
 485 490 495
 Glu Ala Tyr Gly Leu Thr Leu Gln Arg Ala Ala Pro Leu Met Val Arg
 500 505 510
 Pro Ile Pro Arg Leu Leu Ser Ser Ala Tyr Thr Val
 515 520

<210> 84

<211> 525

<212> PRT

<213> Festuca arundinacea

<400> 84

Arg Ser Glu Leu Ala Gly Met Asp Ile Pro Leu Ser Leu Leu Leu Ser
 1 5 10 15
 Thr Leu Ala Ile Ser Ala Thr Ile Cys Tyr Val Phe Phe Arg Ala Gly
 20 25 30
 Lys Gly His Arg Ala Pro Leu Pro Leu Pro Pro Gly Pro Arg Gly Trp
 35 40 45
 Pro Val Leu Gly Asn Leu Pro Gln Leu Gly Gly Lys Thr His Gln Thr
 50 55 60
 Leu His Glu Met Thr Lys Val Tyr Gly Pro Val Leu Arg Leu Arg Phe
 65 70 75 80
 Gly Ser Ser Val Val Val Val Ala Gly Ser Ala Ala Val Ala Glu Gln
 85 90 95
 Phe Leu Arg Thr His Asp Ala Lys Phe Ser Ser Arg Pro Pro Asn Ser
 100 105 110
 Gly Gly Glu His Met Ala Tyr Asn Tyr Arg Asp Val Val Phe Ala Pro
 115 120 125
 Tyr Gly Pro Arg Trp Arg Ala Met Arg Lys Val Cys Ala Val Asn Ile
 130 135 140
 Phe Ser Ala Arg Ala Leu Asp Asp Leu Arg Gly Phe Arg Glu Arg Glu
 145 150 155 160
 Ala Ala Leu Met Val Arg Ser Leu Ala Asp Ala Ala Lys Ala Gly Val
 165 170 175
 Ala Val Ala Val Gly Lys Ala Ala Asn Val Cys Thr Thr Asn Gly Leu
 180 185 190
 Ser Arg Ala Ala Val Gly Leu Arg Val Phe Gly Ser Asp Gly Ala Arg
 195 200 205
 Asp Phe Lys Glu Ile Val Leu Glu Val Met Glu Val Gly Gly Val Leu
 210 215 220
 Asn Val Gly Asp Phe Val Pro Ala Leu Arg Trp Leu Asp Pro Gln Gly
 225 230 235 240
 Val Val Ala Arg Leu Lys Lys Leu His Arg Arg Phe Asp Asp Met Met
 245 250 255
 Asn Gly Ile Ile Ala Glu Arg Arg Thr Gly Thr Lys Thr Ala Val Val
 260 265 270
 Glu Glu Gly Lys Gly Asp Leu Leu Gly Leu Leu Leu Ala Met Val Gln
 275 280 285
 Glu Asp Lys Ser Leu Thr Gly Ser Glu Glu Asp Lys Ile Thr Asp Thr
 290 295 300
 Asp Val Lys Ala Leu Ile Leu Asn Leu Phe Val Ala Gly Thr Glu Thr
 305 310 315 320
 Thr Ser Ser Ile Val Glu Trp Ala Val Ala Glu Leu Ile Arg His Pro
 325 330 335
 Asp Ile Leu Lys Gln Ala Gln Glu Glu Leu Asp Ala Val Val Gly Arg
 340 345 350
 Asp Arg Leu Val Ser Glu Ser Asp Leu Pro Arg Leu Thr Phe Phe Asn

Ala	Ile	Ile	Lys	Glu	Thr	Phe	Arg	Leu	His	Pro	Ser	Thr	Pro	Leu	Ser
355						360						365			
370						375						380			
Leu	Pro	Arg	Met	Ala	Ser	Glu	Glu	Cys	Glu	Val	Ala	Gly	Tyr	His	Ile
385						390						395			400
Pro	Arg	Gly	Thr	Glu	Leu	Leu	Val	Asn	Val	Trp	Gly	Ile	Ala	Arg	Asp
												405			415
Pro	Ala	Leu	Trp	Pro	Asp	Pro	Leu	Glu	Tyr	Gln	Pro	Ala	Arg	Phe	Leu
												420			430
Pro	Gly	Gly	Ser	His	Glu	Asn	Val	Asp	Leu	Lys	Gly	Gly	Asp	Phe	Gly
												435			445
Leu	Ile	Pro	Phe	Gly	Ala	Gly	Arg	Arg	Ile	Cys	Ala	Gly	Leu	Ser	Trp
												450			460
Gly	Leu	Arg	Met	Val	Thr	Ile	Thr	Thr	Ala	Thr	Leu	Val	His	Ser	Phe
465						470						475			480
Asp	Trp	Glu	Leu	Pro	Ala	Gly	Gln	Thr	Pro	Asp	Lys	Leu	Asn	Met	Glu
												485			495
Glu	Ala	Phe	Ser	Leu	Leu	Leu	Gln	Arg	Ala	Val	Pro	Leu	Met	Val	His
												500			510
Pro	Val	Pro	Arg	Leu	Leu	Pro	Ser	Ala	Tyr	Glu	Ile	Ser			
												515			525

<210> 85

<211> 526

<212> PRT

<213> Festuca arundinacea

<400> 85

Met	Arg	Ser	Glu	Leu	'Ala	Gly	Met	Asp	Ile	Pro	Leu	Pro	Leu	Leu	Leu	
1					5					10				15		
Ser	Thr	Leu	'Ala	Ile	Ser	Ala	Thr	Ile	Cys	Tyr	Val	Phe	Phe	Arg	'Ala	
										25				30		
Gly	Lys	Gly	His	Arg	Ala	Pro	Leu	Pro	Leu	Pro	Pro	Gly	Pro	Arg	Gly	
												35		40	45	
Trp	Pro	Val	Leu	Gly	Asn	Leu	Pro	Gln	Leu	Gly	Gly	Lys	Thr	His	Gln	
												50		55	60	
Thr	Leu	His	Glu	Met	Thr	Lys	Val	Tyr	Gly	Pro	Val	Leu	Arg	Leu	Arg	
65												65		70	75	80
Phe	Gly	Ser	Ser	Val	Val	Val	Val	Ala	Gly	Ser	Ala	Ala	Val	Ala	Glu	
												85		90	95	
Gln	Phe	Leu	Arg	Thr	His	Asp	Ala	Lys	Phe	Ser	Ser	Arg	Pro	Pro	Asn	
												100		105	110	
Ser	Gly	Gly	Glu	His	Met	Ala	Tyr	Asn	Tyr	Arg	Asp	Val	Val	Phe	'Ala	
												115		120	125	
Pro	Tyr	Gly	Pro	Arg	Trp	Arg	Ala	Met	Arg	Lys	Val	Cys	'Ala	Val	Asn	
												130		135	140	
Ile	Phe	Ser	Ala	Arg	'Ala	Leu	Asp	Asp	Leu	Arg	Gly	Phe	Arg	Glu	Arg	
												145		150	155	160
Glu	Ala	Ala	Leu	Met	Val	Arg	Ser	Leu	'Ala	Asp	Ala	Ala	Lys	Ala	Gly	
												165		170	175	
Val	Ala	Val	Ala	Val	Gly	Lys	Ala	Ala	Asn	Val	Cys	Thr	Thr	Asn	Gly	
												180		185	190	
Leu	Ser	Arg	Ala	Ala	Val	Gly	Leu	Arg	Val	Phe	Gly	Ser	Asp	Gly	'Ala	
												195		200	205	
Arg	Asp	Phe	Lys	Glu	Ile	Val	Leu	Glu	Val	Met	Glu	Val	Gly	Gly	Val	
												210		215	220	
Leu	Asn	Val	Gly	Asp	Phe	Val	Pro	'Ala	Leu	Arg	Trp	Leu	Asp	Pro	Gln	
												225		230	235	240
Gly	Val	Val	Ala	Arg	Leu	Lys	Lys	Leu	His	Arg	Arg	Phe	Asp	Asp	Met	
												245		250	255	
Met	Asn	Gly	Ile	Ile	'Ala	Glu	Arg	Arg	Gly	Thr	Lys	Thr	'Ala	Val		
												260		265	270	
Val	Glu	Glu	Gly	Lys	Gly	Asp	Leu	Leu	Gly	Leu	Leu	Leu	Ala	Met	Val	
												275		280	285	
Gln	Glu	Asp	Lys	Ser	Leu	Thr	Gly	Ser	Glu	Glu	Asp	Lys	Ile	Thr	Asp	
												290		295	300	
Thr	Asp	Val	Lys	Ala	Leu	Ile	Leu	Asn	Leu	Phe	Val	'Ala	Gly	Thr	Glu	
												305		310	315	320

Thr Thr Ser Ser Ile Val Glu Trp Ala Val Ala Glu Leu Ile Arg His
 325 330 335
 Pro Asp Ile Leu Lys Gln Ala Gln Glu Glu Leu Asp Ala Val Val Gly
 340 345 350
 Arg Asp Arg Leu Val Ser Glu Ser Asp Leu Pro Arg Leu Thr Phe Phe
 355 360 365
 Asn Ala Ile Ile Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro Leu
 370 375 380
 Ser Leu Pro Arg Met Ala Ser Glu Glu Cys Glu Val Ala Gly Tyr His
 385 390 395 400
 Ile Pro Arg Gly Thr Glu Leu Leu Val Asn Val Trp Gly Ile Ala Arg
 405 410 415
 Asp Pro Ala Leu Trp Pro Asp Pro Leu Glu Tyr Gln Pro Ala Arg Phe
 420 425 430
 Leu Pro Gly Gly Ser His Glu Asn Val Asp Leu Lys Gly Gly Asp Phe
 435 440 445
 Gly Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Leu Ser
 450 455 460
 Trp Gly Leu Arg Met Val Thr Ile Thr Thr Ala Thr Leu Val His Ser
 465 470 475 480
 Phe Asp Trp Glu Leu Pro Ala Gly Gln Thr Pro Asp Lys Leu Asn Met
 485 490 495
 Glu Glu Ala Phe Ser Leu Leu Leu Gln Arg Ala Val Pro Leu Met Val
 500 505 510
 His Pro Val Pro Arg Leu Leu Pro Ser Ala Tyr Glu Ile Ser
 515 520 525

<210> 86

<211> 491

<212> PRT

<213> Festuca arundinacea

<400> 86

Asp Ile Pro Leu Pro Leu Leu Ser Thr Leu Ala Ile Ser Ala Thr
 1 5 10 15
 Ile Cys Tyr Val Phe Phe Arg Ala Gly Lys Thr His Gln Thr Leu His
 20 25 30
 Glu Met Thr Lys Val Tyr Gly Pro Val Leu Arg Leu Arg Phe Gly Ser
 35 40 45
 Ser Val Val Val Val Ala Gly Ser Ala Ala Val Ala Glu Gln Phe Leu
 50 55 60
 Arg Thr His Asp Ala Lys Phe Ser Ser Arg Pro Pro Asn Ser Gly Gly
 65 70 75 80
 Glu His Met Ala Tyr Asn Tyr Gln Asp Ile Val Phe Ala Pro Tyr Gly
 85 90 95
 Pro Arg Trp Arg Ala Met Arg Lys Val Cys Ala Val Asn Ile Phe Ser
 100 105 110
 Ala Arg Ala Leu Asp Asp Leu Arg Gly Phe Arg Glu Arg Glu Ala Ala
 115 120 125
 Leu Met Val Arg Ser Leu Ala Asp Ala Ala Lys Ala Gly Ala Ala Val
 130 135 140
 Ala Val Gly Lys Ala Ala Asn Val Cys Thr Thr Asn Gly Leu Ser Arg
 145 150 155 160
 Ala Ala Val Gly Leu Arg Val Phe Gly Ser Asp Gly Thr Arg Asp Phe
 165 170 175
 Lys Glu Ile Val Leu Glu Val Met Glu Val Gly Gly Val Leu Asn Val
 180 185 190
 Gly Asp Phe Val Pro Ala Leu Arg Trp Leu Asp Pro Gln Gly Val Val
 195 200 205
 Ala Arg Met Lys Lys Leu His Arg Arg Phe Asp Asp Ile Met Asn Gly
 210 215 220
 Ile Ile Ala Glu Arg Arg Thr Gly Ala Lys Thr Ala Val Val Glu Glu
 225 230 235 240
 Gly Lys Gly Asp Leu Leu Gly Leu Leu Leu Ala Met Val Gln Glu Asp
 245 250 255
 Lys Ser Leu Thr Gly Ser Glu Glu Asp Lys Ile Thr Asp Thr Asp Val
 260 265 270
 Lys Ala Leu Ile Leu Asn Leu Phe Val Ala Gly Thr Glu Thr Thr Ser

Ser	Ile	Val	Glu	Trp	Ala	Val	275	280	285
290			295		300				
Leu	Lys	Gln	Ala	Gln	Glu	Glu	305	310	315
					Leu	Asp	310	315	320
					Thr	Val			
						Val			
Ile	Val	Ser	Glu	Ser	Asp	Leu	Pro	Arg	
						Leu	Thr	Phe	
							Phe	Asn	
								Ala	Ile
									335
Ile	Lys	Glu	Thr	Phe	Arg	Leu	His	Pro	
							Pro	Ser	
							Thr	Thr	
							Pro	Leu	
Arg	Met	Ala	Ser	Glu	Asp	Cys	340	345	350
						Glu	Val	Ala	Gly
							355	360	Tyr
Gly	Thr	Glu	Leu	Leu	Val	Asn	365	370	His
					Val	Val	370	375	Ile
						Trp		380	Pro
Leu	Trp	Pro	Asp	Pro	Leu	Glu	385	390	Asp
						Tyr		395	Pro
						Arg			Gly
Gly	Ser	His	Glu	Asn	Val	Asp	405	410	Leu
						Leu			Ile
						Lys			415
Pro	Phe	Gly	Ala	Gly	Arg	Arg	420	425	430
						Ile			
						Cys			
						Ala			
Arg	Met	Val	Thr	Val	Thr	Thr	425	430	
						Ala			
						Thr			
						Leu			
Glu	Leu	Pro	Ala	Gly	Gln	Thr	435	440	
						Leu			
						Asp			
Phe	Ser	Leu	Leu	Leu	Gln	Arg	440	445	
						Ala			
						Met			
445	450	455	460	465	470	475	475	480	
Pro	Arg	Leu	Leu	Pro	Ser	Ala	Tyr	Glu	Ile
									Ser
									485
									490

<210> 87

<211> 499

<212> PRT

<213> Festuca arundinacea

<400> 87

Met	Arg	Asn	Glu	Leu	Ala	Gly	Met	Asp	Ile	Pro	Leu	Pro	Leu	Leu
1				5			10				15			
Ser	Thr	Leu	Ala	Ile	Ser	Ala	20	Thr	Ile	Cys	Tyr	Val	Phe	Phe
							25				30			
Gly	Lys	Thr	His	Gln	Thr	Leu	His	Glu	Met	Thr	Lys	Val	Tyr	Gly
							35	40			45			
Val	Leu	Arg	Leu	Arg	Phe	Gly	50	Ser	Ser	Val	Val	Val	Val	Ala
							55				60			Gly
Ala	Ala	Val	Ala	Glu	Gln	Phe	65	Leu	Arg	Thr	His	Asp	Ala	Lys
							70			75		80		Phe
Ser	Arg	Pro	Pro	Asn	Ser	Gly	85	Glu	His	Met	Ala	Tyr	Asn	Tyr
							90				95			Gln
Asp	Ile	Val	Phe	Ala	Pro	Tyr	100	Gly	Pro	Arg	Trp	Arg	Ala	Met
							105				110			Arg
Val	cys	Ala	Val	Asn	Ile	Phe	115	Ser	Ala	Arg	Ala	Leu	Asp	Asp
							120				125			Leu
Gly	Phe	Arg	Glu	Arg	Glu	Ala	130	Ala	Leu	Met	Val	Arg	Ser	Leu
							135				140			Ala
Ala	Ala	Lys	Ala	Gly	Ala	Ala	145	Val	Ala	Val	Gly	Lys	Ala	Ala
							150				155			Asn
Cys	Thr	Thr	Asn	Gly	Leu	Ser	165	Arg	Ala	Ala	Val	Gly	Leu	Arg
							170					175		Phe
Gly	Ser	Asp	Gly	Thr	Arg	Asp	180	Phe	Lys	Glu	Ile	Val	Leu	Glu
							185					190		Val
Glu	Val	Gly	Gly	Val	Leu	Asn	195	Gly	Asp	Phe	Val	Pro	Ala	Leu
							200				205			Arg
Trp	Leu	Asp	Pro	Gln	Gly	Val	210	Val	Ala	Arg	Met	Lys	Lys	Leu
							215				220			His
Arg	Phe	Asp	Asp	Ile	Met	Asn	225	Gly	Ile	Ile	Ala	Glu	Arg	Arg
							230				235			Thr
Ala	Lys	Thr	Ala	Val	Val	Glu	245	Gly	Lys	Gly	Asp	Leu	Leu	Gly
							250					255		Leu
Leu	Leu	Ala	Met	Val	Gln	Glu	260	Asp	Lys	Ser	Leu	Thr	Gly	Ser
							265					270		Glu

Asp Lys Ile Thr Asp Thr Asp Val Lys Ala Leu Ile Leu Asn Leu Phe
 275 280 285
 Val Ala Gly Thr Glu Thr Thr Ser Ser Ile Val Glu Trp Ala Val Ala
 290 295 300
 Glu Leu Ile Arg His Pro Asp Ile Leu Lys Gln Ala Gln Glu Glu Leu
 305 310 315 320
 Asp Thr Val Val Gly Arg Asp Arg Ile Val Ser Glu Ser Asp Leu Pro
 325 330 335
 Arg Leu Thr Phe Phe Asn Ala Ile Ile Lys Glu Thr Phe Arg Leu His
 340 345 350
 Pro Ser Thr Pro Leu Ser Leu Pro Arg Met Ala Ser Glu Asp Cys Glu
 355 360 365
 Val Ala Gly Tyr His Ile Pro Arg Gly Thr Glu Leu Leu Val Asn Val
 370 375 380
 Trp Gly Ile Ala Arg Asp Pro Ser Leu Trp Pro Asp Pro Leu Glu Tyr
 385 390 395 400
 Arg Pro Ala Arg Phe Leu Pro Gly Gly Ser His Glu Asn Val Asp Leu
 405 410 415
 Lys Gly Gly Asp Phe Gly Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile
 420 425 430
 Cys Ala Gly Leu Ser Trp Gly Leu Arg Met Val Thr Val Thr Thr Ala
 435 440 445
 Thr Leu Val His Ser Phe Asp Trp Glu Leu Pro Ala Gly Gln Thr Leu
 450 455 460
 Asp Lys Leu Asn Met Glu Glu Ala Phe Ser Leu Leu Leu Gln Arg Ala
 465 470 475 480
 Met Pro Leu Met Val His Pro Val Pro Arg Leu Leu Pro Ser Ala Tyr
 485 490 495
 Glu Ile Ser

<210> 88
 <211> 380
 <212> PRT
 <213> *Lolium perenne*

<400> 88
 Met Ala Met Ala Asp Cys Met Gln Glu Trp Pro Glu Pro Val Val Arg
 1 5 10 15
 Val Gln Ala Val Ala Glu Ser Gly Leu Ala Ala Ile Pro Asp Cys Tyr
 20 25 30
 Val Lys Pro Pro Arg Asp Arg Pro Ala Ala Gln His Leu Ala Thr Ala
 35 40 45
 Ala Ser Ala Asp Gly Asp Val Leu His Glu Pro Leu Asp Thr Ser Ile
 50 55 60
 Pro Val Ile Asp Leu Gly Glu Leu Val Ala Ala Thr Ala Asp Glu Gly
 65 70 75 80
 Arg Met Arg Gln Ile Met Glu Ala Val Ala Ala Ala Cys Arg Glu Trp
 85 90 95
 Gly Phe Phe Gln Val Val Asn His Gly Val Ala Pro Glu Leu Met His
 100 105 110
 Ala Ala Arg Glu Ala Trp Arg Gly Phe Phe Arg Leu Pro Ile Thr Ala
 115 120 125
 Lys Gln Gln Tyr Ala Asn Leu Pro Arg Thr Tyr Glu Gly Tyr Gly Ser
 130 135 140
 Arg Val Gly Val Gln Lys Gly Gly Pro Leu Asp Trp Gly Asp Tyr Tyr
 145 150 155 160
 Phe Leu His Leu Ala Pro Asp Ala Gly Lys Ser Pro Asp Lys Tyr Trp
 165 170 175
 Pro Thr Asn Pro Ala Ile Cys Lys Asp Val Ser Glu Glu Tyr Gly Arg
 180 185 190
 Glu Val Ile Arg Leu Cys Glu Leu Leu Met Lys Val Met Ser Ala Ser
 195 200 205
 Leu Gly Leu Glu Ala Thr Arg Phe Gln Glu Ala Phe Gly Gly Ser Glu
 210 215 220
 Cys Gly Val Cys Leu Arg Ala Asn Tyr Tyr Pro Arg Cys Pro Gln Pro
 225 230 235 240
 Asp Leu Thr Leu Gly Leu Ser Ala His Ser Asp Pro Gly Val Leu Thr

245	250	255	
Val Leu Leu Ala Asp Glu His Val Arg Gly Leu Gln Val Arg Arg Ala			
260	265	270	
Asp Gly Glu Trp Val Thr Val Gln Pro Ala Arg His Asp Ala Phe Ile			
275	280	285	
Val Asn Val Gly Asp Gln Ile Gln Ile Leu Ser Asn Ser Met Tyr Lys			
290	295	300	
Ser Val Glu His Arg Val Met Val Asn Ala Lys Glu Glu Arg Ile Ser			
305	310	315	320
Leu Ala Leu Phe Tyr Asn Pro Arg Gly Asp Val Pro Ile Ala Pro Ala			
325	330	335	
Pro Glu Thr Val Thr Pro Glu Arg Pro Ala Leu Tyr Pro Ser Met Thr			
340	345	350	
Phe Asp Glu Tyr Arg Ala Tyr Ile Arg Lys Tyr Gly Pro Arg Gly Lys			
355	360	365	
Ala Gln Val Glu Gly Ala Lys Gln Gly Gln Gly Ser			
370	375	380	

<210> 89

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in the lab

<400> 89

gacgcaagga gagatccaga

20

<210> 90

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in the lab

<400> 90

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20

<210> 91

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in the lab

<400> 91

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26

<210> 92

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in the lab

<400> 92

gccgaacaga ccattgaagt a

21

INTERNATIONAL SEARCH REPORT

International application No.

PCT/NZ03/00081

A. CLASSIFICATION OF SUBJECT MATTER

Int. Cl. 7: C12N 9/10, 9/02, 5/14, 15/82, C07K 14/415, A01H 5/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
 See electronic database box below.

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
 See electronic database box below.

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
 DGENE, EMBL, GenBank, PDB, DDBJ, USPTO sequences: SEQ ID NO: 4, 12, 15, 15, 17, 20, 22, 27, 33, 35, 37.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	EMBL database Accession Number AF492836 & AAM13671. Lasseur B <i>et al.</i> 16 April 2002. "Lolium perenne putative sucrose:sucrose 1-fructosyltransferase mRNA, complete cds". See whole document. 97.8% identical to SEQ ID NOs: 4 and 48.	1-25 (SEQ ID NO: 4 & 48)
X	Luscher M <i>et al.</i> (2000) Plant Physiol. 124(3):1217-28. "Cloning and functional analysis of sucrose:sucrose 1-fructosyltransferase from tall fescue". & EMBL database Accession Number AJ297369 & CAC05261. See whole document. 83% identical to SEQ ID NO: 4 and 48.	1-25 (SEQ ID NO: 4 & 48)

 Further documents are listed in the continuation of Box C See patent family annex

* Special categories of cited documents:		
"A" document defining the general state of the art which is not considered to be of particular relevance	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"E" earlier application or patent but published on or after the international filing date	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"O" document referring to an oral disclosure, use, exhibition or other means	"&"	document member of the same patent family
"P" document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search
 22 August 2003

Date of mailing of the international search report

27 Aug 2003

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/NZ03/00081

Box I Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos :
because they relate to subject matter not required to be searched by this Authority, namely:

2. Claims Nos :
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. Claims Nos :
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a)

Box II Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

See extra sheet below.

1. As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:1-25 (in part).

Remark on Protest The additional search fees were accompanied by the applicant's protest. No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/NZ03/00081

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages <i>(Remove spaces when completed if the page is too long)</i>	Relevant to claim No.
X	WO 01/95691, A (State of Victoria, Department of Natural Resources and Environment <i>et al.</i>) 20 December 2001. See whole document. SST (Figure 11 & SEQ ID NO: 11) is 95% identical to SEQ ID NO: 4.	1-25 (SEQ ID NOs: 4 & 48)
X	WO 02/31130, A (Agriculture Victoria Services Pty Ltd & AGRESEARCH Ltd) 18 April 2002. See whole document. SST (figure 56) is 95% identical to SEQ ID NO: 4. SFT (figure 61) is 98% identical to SEQ ID NO: 4. INV (figure 20) is 64.4% identical to SEQ ID NO: 12. SPS (figures 5, 15 and 17) are 96-99% identical to SEQ ID NO: 20. ST (figures 47 and 49) are 94-96.5% identical to SEQ ID NO: 22.	1-25 (SEQ ID NOs: 4 & 48, 12 & 56, 20 & 64, 22 & 66)
X	US 2001/0051335, A (Lalgudi R V <i>et al.</i>) 13 December 2001. See whole document. SEQ ID NO: 5640 is 86.4% identical to SEQ ID NO: 12. SEQ ID NOs: 745 & 4804 are 85.7% and 87.5% respectively identical to SEQ ID NO: 15. SEQ ID NO: 5903 is 83.5% identical to SEQ ID NO: 27.	2-4, 6-10, 12, 13. (SEQ ID NO: 12 & 56, 15 & 59, 27 & 71)
X	EP 1033405, A (Ceres Incorporated Malibu) 6 September 2000. See whole document. SEQ ID NO: 11557 is 74% identical to SEQ ID NO: 12. SEQ ID NO: 43076 & 48532 are 81.3% and 73.3 % respectively identical to SEQ ID NO: 17. SEQ ID NO: 20393 is 38.8% identical to SEQ ID NO: 37, also 100% match over 21 nucleotides (nt100-120 of SEQ ID NO: 20393 matches nt555-575 of SEQ ID NO: 37).	2-4, 6-16. (SEQ ID NO: 12 & 56, 17 & 61, 37 & 81)
X	EMBL database Accession Number: AF095521 & AAC67587. Kapri R & Sadka A. 26 October 1998. "Citrus X paradisi pyrophosphate-dependent phosphofructokinase alpha subunit (PPi-PFKa) mRNA, complete cds". See whole document. 70.6% identical to SEQ ID NO: 15 over entire length, 83% identical over 407 nucleotides (nt 634-1040).	1-25. (SEQ ID NO: 15 & 59)
X	Carlisle S M <i>et al.</i> (1990) J Biol. Chem. 265(30): 18366-18371. "Pyrophosphate-dependent phosphofructokinase. Conservation of protein sequence between the alpha- and beta-subunits and with the ATP-dependent phosphofructokinase" & EMBL database Accession Number: M55190 & AAA63451 and M55191 & AAA63452. See whole document. 70.7% identical to SEQ ID NO: 15. 78% identical to SEQ ID NO: 17.	1-25. (SEQ ID NO: 15 & 59, 17 & 61))

INTERNATIONAL SEARCH REPORT

International application No.

PCT/NZ03/00081

C (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages <i>(Remove spaces when completed if the page is too long)</i>	Relevant to claim No.
X	WO 02/16655, A (The Scripps Research Institute <i>et al.</i>) 28 February 2002. See whole document. SEQ ID NO: 2691 is 72.2% identical to SEQ ID NO: 15. SEQ ID NO: 188 is 73.3% identical to SEQ ID NO: 17.	1-25 (SEQ ID NO: 15 & 59, 17& 61)
P, X	US 6476212, B (Lalgudi, R V <i>et al.</i>) 5 November 2002. See whole document. SEQ ID NO: 584, 1329, 3963, 7175 are 86%, 93%, 87% and 85% identical to SEQ ID NO: 15 respectively.	2-4, 6-14. (SEQ ID NO: 15 & 59)
X	EMBL database Accession Number: AF095520 & AAC67586. Kapri R & Sadka A. 26 October 1998. "Citrus X paradisi pyrophosphate-dependent phosphofructokinase beta subunit (PPi-PFKb) mRNA, complete cds". See whole document. 37.7% identical to SEQ ID NO: 17 over entire length, 82% identical over 620 nucleotides (nt 513-1132 matches nt 541-1160 of SEQ ID NO: 17)	1-25. (SEQ ID NO: 17 & 61)
X	US 2002/0042930, A (Botha F C & Groenewald J H) 11 April 2002. See whole document. Especially figure 2 And SEQ ID NO: 2 83.2% identical to SEQ ID NO: 17.	1-25 (SEQ ID NO: 17 & 61)
P, X	WO 03/000905, A (SYNGENTA PARTICIPATIONS AG) 3 January 2003. See whole document. SEQ ID NO: 179, 587, 1002 are 92%, 87% & 87% identical to SEQ ID NO: 17 respectively.	1-25 (SEQ ID NO: 17 & 61)
X	EMBL database Accession Number: AF261107 & AAF75266. Lunn J E <i>et al.</i> 11 June 2000. "Hordeum vulgare sucrose-phosphate synthase mRNA, partial cds". See whole document. 88.6% identical to SEQ ID NO: 20.	1-25 (SEQ ID NO: 20 & 64)
X	WO 99/57285, A (E.I. DU PONT DE NEMOURS AND COMPANY) 11 November 1999. See whole document. SEQ ID NO: 9 & 19 are 85% & 85.4% identical to SEQ ID NO: 20 respectively.	1-25 (SEQ ID NO: 20 & 64)
X	EMBL database Accession Number: AJ272309 & CAB75882. Weschke W <i>et al.</i> 22 February 2000. "Hordeum vulgare mRNA for sucrose transporter 1 (Sut1 gene)" See whole document. 83.6% identical to SEQ ID NO: 22.	1-25 (SEQ ID NO: 22 & 66)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/NZ03/00081

C (Continuation)		DOCUMENTS CONSIDERED TO BE RELEVANT
Category*	Citation of document, with indication, where appropriate, of the relevant passages <i>(Remove spaces when completed if the page is too long)</i>	Relevant to claim No.
X	EMBL database Accession Numbers: AF408842, AF408843 & AF408844 (& AAM13408, AAM13409 & AAM13410). Aoki N <i>et al.</i> 16 April 2002. "Triticum aestivum sucrose transporter SUT1A, SUT1B, SUT1D mRNA, complete cds" See whole documents. AF408842 is 82.8% identical to SEQ ID NO: 22. AF408843 is 82.9% identical to SEQ ID NO: 22. AF408844 is 81.8% identical to SEQ ID NO: 22.	1-25 (SEQ ID NO: 22 & 66)
X	WO 99/53068, A ((E.I. DU PONT DE NEMOURS AND COMPANY) 21 October 1999. See whole document, especially SEQ ID NO: 19-22. SEQ ID NO: 19 & 21 are 81.5% & 83% identical to SEQ ID NO: 22.	1-25 (SEQ ID NO: 22 & 66)
X	WO 01/64890, A (Pioneer Hi-Bred International, Inc.) 7 September 2001. See whole document, see SEQ ID NO: 8. SEQ ID NO: 8 is 63.3% identical to SEQ ID NO: 27.	2-4, 6-16 (SEQ ID NO: 27 & 71)
X	EMBL database Accession Number: X92547 & CAA63305. Haussuehl K K <i>et al.</i> 12 August 1996. "S. cereale mRNA for chalcone synthase". See whole document. 85.5% identical to SEQ ID NO: 33.	1-25 (SEQ ID NO: 33 & 77)
X	EMBL database Accession Number: X58339 & CAA41250. Rohde W E <i>et al.</i> 7 November 1991. "H. vulgare CHS gene for chalcone synthase". See whole document. 74.8% identical to SEQ ID NO: 33.	1-25 (SEQ ID NO: 33 & 77)
X	EMBL database Accession Number: AB000801 & BAA19186. Ichikawa H <i>et al.</i> 27 March 2001. "Oryza sativa mRNA for chalcone synthase, complete cds". See whole document. 76.3% identical to SEQ ID NO: 33.	1-25 (SEQ ID NO: 33 & 77)
X	WO 02/20548, A (Washington State University Research Foundation) 14 March 2002. See whole document., especially SEQ ID NO:25 SEQ ID NO: 25 is 79.3% identical to SEQ ID NO: 33.	1-25 (SEQ ID NO: 33 & 77)
P, X	WO 02/086146, A (Cornell Research Foundation Inc.) 31 October 2002. See whole document. SEQ ID NO: 46 is 92.4% identical to SEQ ID NO: 33.	1-25 (SEQ ID NO: 33 & 77)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/NZ03/00081

C (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages <i>(Remove spaces when completed if the page is too long)</i>	Relevant to claim No.
X	GENPEPT & GENBANK database Accession Numbers: AAF23859 & AF092912. Devic M <i>et al.</i> 11 January 2000. "DFR-like protein [Arabidopsis thaliana]". See whole document. 45.6% identity & 63.6% similarity with SEQ ID NO: 79 43.2% identity & 67.2% similarity with SEQ ID NO: 81	1-25 (SEQ ID NO: 35 & 79, 37 & 81)
X	GENPEPT & GENBANK database Accession Numbers: CAA75998 & Y16042. Bernhardt J <i>et al.</i> 30 June 1998. "Dihydroflavonol4-reductase [zea mays]". See whole document. 39.3% identity & 61.6% similarity with SEQ ID NO: 79 38.3% identity & 64.7% similarity with SEQ ID NO: 81	1-25 (SEQ ID NO: 35 & 79, 37 & 81)
X	GENPEPT & GENBANK database Accession Numbers: BAA12723 & D85102. Tanaka Y <i>et al.</i> 6 February 1999. "Dihydroflavonol 4-reductase [Rosa hybrid cultivar]". See whole document. 39% identity & 60.9% similarity with SEQ ID NO: 79 40.2% identity & 65% similarity with SEQ ID NO: 81	1-25 (SEQ ID NO: 35 & 79, 37 & 81)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/NZ03/00081

Supplemental Box

(To be used when the space in any of Boxes I to VIII is not sufficient)

Continuation of Box No: II

The international application does not comply with the requirements of unity of invention because it does not relate to one invention or to a group of inventions so linked as to form a single general inventive concept. The fundamental test for unity of invention is specified in Rule 13.2 of the Regulations under the PCT.

"Where a group of inventions is claimed in one and the same international application, the requirement of unity of invention referred to in Rule 13.1 shall be fulfilled only where there is a technical relationship among those inventions involving one or more of the same or corresponding special technical features. The expression "special technical feature" shall mean those technical features that define a contribution which each of the claimed inventions, considered as a whole, make over the prior art."

In the case of the present application, the problem addressed by the application is the need in the art for materials useful in the modification of fructan and tannin content and composition in plants. The solution provided by the applicant is to provide enzymes involved in the fructan, cellulose, starch and/or tannin biosynthetic pathways isolated from forage grass tissues. Specifically, the solutions provided are in the form of 44 specific enzymes from ryegrass or fescue species and the nucleic acids or fragments coding for these enzymes. These 44 specific polypeptides fall within general groupings dependent upon which pathway they appear in (Table 1 pages 17-21). Such groupings do not confer a "special technical feature" in terms of their function.

The protein groups do share the feature of being from the plant species *Lolium* (ryegrass) or *Festuca* (fescue). However the species of origin can only constitute a special technical feature if the species or origin makes a contribution over the prior art. There is nothing in the application to indicate that isolation of peptides from fescue or ryegrass is inventive. It was known that enzymes belonging to these families would be present in ryegrass and fescue (by analogy with other plant species). The presence of these enzymes in other plant species is known in the prior art.

Therefore, none of the enzymes have any functional feature that can be seen as a "special technical feature" in common. Furthermore, none of the sequences claimed appear to have any significant homology to one another that would provide for a "special technical feature" based upon structure. Finally, none of the sequences claimed can be searched without requiring significant extra effort.

Therefore, this application is directed towards 44 separate inventions. As a service to the Applicant the ISA has searched ten separate inventions for the one fee. The Applicant selected ten sequences to be searched. The ten selected nucleotide sequences and their corresponding protein sequences that were searched are:

SEQ ID NO: 4 and 48

EQ ID NO: 12 and 56

SEQ ID NO: 15 and 59

SEQ ID NO: 17 and 61

SEQ ID NO: 20 and 64

SEQ ID NO: 22 and 66

SEQ ID NO: 27 and 71

SEQ ID NO: 33 and 77

SEQ ID NO: 35 and 79

SEQ ID NO: 37 and 81.

INTERNATIONAL SEARCH REPORT

PCT/NZ03/00081

This Annex lists the known "A" publication level patent family members relating to the patent documents cited in the above-mentioned international search report. The Australian Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

Patent Document Cited in Search Report			Patent Family Member				
			(To put a line under the citations tab to the first point on the next row and press F8)				
WO	200195691	AU	20008155	AU	200165676	EP	1305420
WO	200231130	AU	20000673	AU	200195256		
US	2001005133	EP	1083408	JP	2001082915	US	6304076
		US	2002000129	EP	1225426	JP	2002340611
		EP	1134567	JP	2001304984		
EP	1033405		NONE				
WO	200216655	AU	200186811	CA	2420555	EP	131867
US	2002042930	AU	200118335	BR	200100470	CN	1344799
		FR	2806741				
US	6476212		NONE				
WO	2003000905	WO	2003000897	WO	2003000904	WO	2003000906
		WO	2003007699	WO	2003008540	US	2003135888
		WO	2003027249				
WO	9957285	AU	37880/99	BR	9910343	CA	2326382
		EP	1076709	US	6323015	US	2002090704
WO	9953068	AU	34748/99	EP	1070130		
WO	200164890	AU	200141622	US	2002004940	US	2003140369
WO	200220548	AU	200188741	CA	2421911	US	2002174452
WO	2002086146		NONE				

END OF ANNEX